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OM protein - protein search, using sw model

Run on: October 14, 2005, 15:51:19 ; Search time 38.4375 Seconds
(without alignments)
50.310 Million cell updates/sec

Title: US-10-614-959-10

Perfect score: 29

Sequence: 1 TYAMH 5

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	5	3 AAY79068	Aay79068 Anti-fact
2	29	100.0	7	3 AAB14789	Aab14789 Aspergill
3	29	100.0	7	3 AAB14784	Aab14784 Aspergill
4	29	100.0	12	4 AAG65570	Aag65570 Amino aci
5	29	100.0	121	5 ABG76537	Abg76537 HCV El an
6	29	100.0	128	5 ABG76559	Abg76559 HCV El an
7	29	100.0	206	6 ABU24807	Abu24807 Protein e
8	29	100.0	258	7 ABO77482	Abu77482 Pseudomon
9	29	100.0	278	8 ADN27332	Adn27332 Bacterial
10	29	100.0	307	4 AAG72483	Aag72483 Human OR-
11	29	100.0	321	4 AAG71475	Aag71475 Human olf
12	29	100.0	531	8 ADRI0293	Adri0293 Human pro
13	29	100.0	690	3 AAY50844	Aay50844 A. oryzae
14	29	100.0	690	3 AAY50835	Aay50835 A. oryzae
15	29	100.0	703	3 AAB14781	Aab14781 Aspergill
16	29	100.0	703	3 AAB14782	Aab14782 Aspergill
17	26	89.7	46	4 AAM82576	Aam82576 Human imm
18	26	89.7	67	4 ABB40299	Abb40299 Peptide #
19	26	89.7	67	4 AAM33985	Aam33985 Peptide #
20	26	89.7	67	4 AAM73798	Aam73798 Human bon
21	26	89.7	67	4 AAM61093	Aam61093 Human bra
22	26	89.7	67	4 ABG55546	Abg55546 Human liv
23	26	89.7	67	5 ABG43685	Abg43685 Human pep
24	26	89.7	79	4 AAU18208	AAU18208 Novel hum
25	26	89.7	79	5 ABG92629	Abg92629 Human DNA

ALIGNMENTS

RESULT 1

AAV79068

ID AAV79068 standard; peptide; 5 AA.

AC AAY79068;

XX

DT 12-JUN-2000 (first entry)

XX

DE Anti-factor IX/IXa antibody H chain V domain CDR1 amino acid sequence.

XX

KW Complementarity determining region 1; CDR1; antibody; Gla domain;

KW factor IX/IXa; blood coagulation; deep venous thrombosis;

KW arterial thrombosis; unstable angina; post myocardial infarction;

KW coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;

KW percutaneous transluminal coronary angioplasty; PTCA; inflammation;

KW septic shock; hypotension; adult respiratory distress syndrome; ARDS;

KW arterial fibrillation; disseminated intravascular coagulopathy; DIC.

XX Homo sapiens.

OS

PN WO200012562-A1.

XX

XX 09-MAR-2000.

PD

XX 26-AUG-1999; 99WO-US019453.

XX

XX 28-AUG-1998; 98US-0098233P.

PR

PR 03-MAR-1999; 99US-0122767P.

XX

PA (GETH) GENENTECH INC.

XX

PI Adams CW, Devaux B, Eaton DL, Hass PE, Judice JK, Kirchhofer D;

PI Suggett S;

XX

DR WPI; 2000-256595/22.

XX

XX Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-

PT carboxyglutamic acid domains useful as anti-coagulant in thrombosis,

PT stroke, and post myocardial infarction.

XX

PS Claim 2; Fig 2; 84pp; English.

XX

CC This sequence represents a complementarity determining region 1 (CDR1) of the heavy chain variable domain of a human anti-factor IX/IXa Gla domain antibody. Factor IXa is a vitamin K dependent plasma serine protease that participates in the blood coagulation pathways. The Gla domain of factor IXa and its zymogen factor IX contains important structural determinants for interaction with high affinity binding sites on vascular endothelial

Adc25346 Human ext
Abg68752 Cytochrom
Abp01422 Human ORF
Abg68756 Cytochrom
Adc08218 Novel pro
Ade08219 Novel pro
Abb91152 Herbicida
Ada55412 Human pro
Abp46042 Human Bly
Adg96869 Single ch
Abb49910 Listeria
Abu17641 Protein e
Aag94423 C glutami
Aag90014 C glutami
Abo63767 Klabsteli
Adf08003 Bacterial
Ado47242 Rabbit cy
Aae26192 Human cyt
Ade57186 Human Pro
Ade57190 Human Pro

CC cells and platelets. Compositions comprising the antibodies are used for
 CC the treatment or prophylaxis of thrombotic or coagulopathic diseases or
 CC disorders in a mammal for which inhibiting a FIX/IXa mediated event is
 CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
 CC angina, post myocardial infarction, post surgical thrombosis, coronary
 CC artery bypass graft (CABG), percutaneous transluminal coronary
 CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
 CC inflammation, septic shock, hypotension, adult respiratory distress
 CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
 CC coagulopathy (DIC)

XX Sequence 5 AA;

Query Match 100.0%; Score 29; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 |||||
 Db 1 TYAMH 5

RESULT 2
 AAB14789
 ID AAB14789 standard; peptide; 7 AA.

AC AAB14789;

DT 06-DEC-2000 (first entry)

DE Aspergillus oryzae KBN616 glutaminase peptide, SEQ ID NO:12.

KW Glutaminase; Aspergillus oryzae KBN616; glutamic acid synthesis;

KW fermentation; foodstuff production; miso; soy sauce; peptide fragment;
 KW PCR primer design.

OS Aspergillus oryzae.

PN JP2000166547-A.

PD 20-JUN-2000.

PF 07-DEC-1998; 98JP-00347127.

PR 07-DEC-1998; 98JP-00347127.

PA (AICH-) AICHI KEN PREFECTURE.

PA (ICHI-) ICHIBIKI KK.

DR WPI; 2000-477931/42.

PT A new glutaminase and its preparation.

PS Example 2; Page 25; 27pp; Japanese.

CC The invention relates to two novel glutaminases (AAB14781, AAB14782) from
 CC Aspergillus oryzae KBN616 and Aspergillus sojae BA-104 respectively which
 CC have molecular weights of approximately 73 kD (as determined by gel
 CC filtration). The enzymes have an optimum temperature of approximately 50
 CC degrees Celsius, and an optimum pH of about 8.5. The glutaminases
 CC catalyse the conversion of L-glutamine to L-glutamic acid, and may be
 CC used in the production of fermented foodstuffs such as soy sauce and
 CC miso. Sequences AAB14787-B14789 represent fragments of Aspergillus oryzae
 CC KBN616 glutaminase which were used as the basis for the design of
 CC degenerate PCR primers AAA72206, AAA72207 and AAA72209. These primers
 CC were used in the isolation of genomic DNA encoding Aspergillus oryzae
 CC KBN616 (AAA72204)

XX Sequence 7 AA;

Query Match 100.0%; Score 29; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 |||||
 Db 3 TYAMH 7

RESULT 3
 AAB14784
 ID AAB14784 standard; peptide; 12 AA.

AC AAB14784;

DT 06-DEC-2000 (first entry)

DE Aspergillus oryzae KBN616 glutaminase peptide fragment, SEQ ID NO:6.

KW Glutaminase; Aspergillus oryzae KBN616; glutamic acid synthesis;

KW fermentation; foodstuff production; miso; soy sauce;

KW V8 protease digestion.

OS Aspergillus oryzae.

PN JP2000166547-A.

PD 20-JUN-2000.

PF 07-DEC-1998; 98JP-00347127.

PR 07-DEC-1998; 98JP-00347127.

PA (AICH-) AICHI KEN PREFECTURE.

PA (ICHI-) ICHIBIKI KK.

DR WPI; 2000-477931/42.

PT A new glutaminase and its preparation.

PS Example 2; Page 9; 27pp; Japanese.

CC The invention relates to two novel glutaminases (AAB14781, AAB14782) from
 CC Aspergillus oryzae KBN616 and Aspergillus sojae BA-104 respectively which
 CC have molecular weights of approximately 73 kD (as determined by gel
 CC filtration). The enzymes have an optimum temperature of approximately 50
 CC degrees Celsius, and an optimum pH of about 8.5. The glutaminases
 CC catalyse the conversion of L-glutamine to L-glutamic acid, and may be
 CC used in the production of fermented foodstuffs such as soy sauce and
 CC miso. Sequences AAB14784-B14786 represent the N-terminal sequences
 CC determined for three V8 protease fragments (P1-P3) of Aspergillus oryzae
 CC KBN616 glutaminase in an exemplification of the invention

SQ Sequence 12 AA;

Query Match 100.0%; Score 29; DB 3; Length 12;
 Best Local Similarity 100.0%; Pred. No. 6.5;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
 |||||
 Db 7 TYAMH 11

RESULT 4
 AAG65570
 ID AAG65570 standard; protein; 120 AA.

AC AAG65570;

DT 30-NOV-2001 (first entry)

DE Amino acid sequence of protein seq Id No. 95.

XX Gene library; immunoglobulin; antibody library; human.

XX

PT Vaccine comprising a human monoclonal antibody against hepatitis C virus
 XX (HCV) E1 or E2 antigen, useful for treating or preventing HCV infection.
 XX Disclosure; Page 36; 64pp; English.
 XX
 CC The invention relates to a human monoclonal antibody or its antigen
 CC binding fragments, which exhibit immunological binding affinity for a
 CC hepatitis C virus (HCV) E1 antigen, comprising an amino acid sequence
 CC homologous to the binding portion of a human antibody Fab molecule from a
 CC combinatorial antibody library. The vaccine composition comprising the
 CC antibodies or antigen binding fragments against HCV E1 or E2 antigen or
 CC its hypervariable region is useful in treating or preventing HCV
 CC infection in a subject. Sequences ABG76513-ABG76568 represent human
 CC monoclonal antibodies against HCV E1 antigen
 XX
 SQ Sequence 121 AA;
 Query Match 100.0%; Score 29; DB 5; Length 121;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY 1 TYAMH 5
 Db 33 TYAMH 37
 |||||

RESULT 6
 ABG76559
 ID ABG76559 standard; protein; 128 AA.
 XX AC ABG76559;
 XX
 XX 05-NOV-2002 (first entry)
 XX HCV E1 antigen monoclonal antibody #47.
 DE
 XX Human; HCV; hepatitis C virus; E1 antigen; monoclonal antibody; vaccine;
 XX hepatotropic; Fab; hypervariable region; E2 antigen; antibody.
 XX Homo sapiens.
 OS
 XX WO200260954-A1.
 PN
 XX
 XX 08-AUG-2002.
 PD
 XX
 XX 14-JAN-2002; 2002WO-SE000044.
 PF
 XX
 XX 12-JAN-2001; 2001US-0260889P.
 PR
 XX
 XX (KARO-) KAROLINSKA INNOVATIONS AB.
 PA
 XX Drakenberg K, Persson MAA;
 PI
 XX WPI; 2002-608502/65.
 DR
 XX
 XX Vaccine comprising a human monoclonal antibody against hepatitis C virus
 PT (HCV) E1 or E2 antigen, useful for treating or preventing HCV infection.
 PT
 XX
 PS Disclosure; Page 52-53; 64pp; English.
 XX
 CC The invention relates to a human monoclonal antibody or its antigen
 CC binding fragments, which exhibit immunological binding affinity for a
 CC hepatitis C virus (HCV) E1 antigen, comprising an amino acid sequence
 CC homologous to the binding portion of a human antibody Fab molecule from a
 CC combinatorial antibody library. The vaccine composition comprising the
 CC antibodies or antigen binding fragments against HCV E1 or E2 antigen or
 CC its hypervariable region is useful in treating or preventing HCV
 CC infection in a subject. Sequences ABG76513-ABG76568 represent human
 CC monoclonal antibodies against HCV E1 antigen
 XX
 SQ Sequence 128 AA;
 Query Match 100.0%; Score 29; DB 5; Length 128;

Best Local Similarity 100.0%; Pred. No. 77;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
DB 32 TYAMH 36

RESULT 7
ABU24807
ID ABU24807 standard; protein; 206 AA.
XX AC ABU24807;
XX DT 19-JUN-2003 (first entry)
XX DE Protein encoded by Prokaryotic essential gene #10334.
XX KW Antisense; prokaryotic essential gene; cell proliferation; drug design.
XX OS Clostridium botulinum.
XX PN WO200277183-A2.
XX PD 03-OCT-2002.
XX PF 21-MAR-2002; 2002WO-US009107.
XX PR 21-MAR-2001; 2001US-00815242.
XX PR 06-SEP-2001; 2001US-00948993.
XX PR 25-OCT-2001; 2001US-0342923P.
XX PR 08-FEB-2002; 2002US-00072851.
XX PR 06-MAR-2002; 2002US-0362699P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;
XX PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;
XX DR WPI; 2003-029926/02.
XX DR N-PSDB; ACA28677.
XX PT New antisense nucleic acids, useful for identifying proteins or screening
XX PT for homologous nucleic acids required for cellular proliferation to
XX PT isolate candidate molecules for rational drug discovery programs.
XX PS Claim 25; SEQ ID NO 52731; 1766pp; English.
XX CC The invention relates to an isolated nucleic acid comprising any one of
XX CC the 6213 antisense sequences given in the specification where expression
XX CC of the nucleic acid inhibits proliferation of a cell. Also included are:
XX CC (1) a vector comprising a promoter operably linked to the nucleic acid
XX CC encoding a polypeptide whose expression is inhibited by the antisense
XX CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
XX CC polypeptide or its fragment whose expression is inhibited by the
XX CC antisense nucleic acid; (4) an antibody capable of specifically binding
XX CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
XX CC proliferation or the activity of a gene in an operon required for
XX CC proliferation; (7) identifying a compound that influences the activity of
XX CC the gene product or that has an activity against a biological pathway
XX CC required for proliferation, or that inhibits cellular proliferation; (8)
XX CC identifying a gene required for cellular proliferation or the biological
XX CC pathway in which a proliferation-required gene or its gene product lies
XX CC or a gene on which the test compound that inhibits proliferation of an
XX CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
XX CC compound's activity; (11) a culture comprising strains in which the gene
XX CC product is overexpressed or underexpressed; (12) determining the extent
XX CC to which each of the strains is present in a culture or collection of
XX CC strains; or (13) identifying the target of a compound that inhibits the
XX CC proliferation of an organism. The antisense nucleic acids are useful for
XX CC identifying proteins or screening for homologous nucleic acids required
XX CC for cellular proliferation to isolate candidate molecules for rational
XX CC drug discovery programs, or for screening homologous nucleic acids

CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX SQ Sequence 206 AA;

Query Match 100.0%; Score 29; DB 6; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
DB 30 TYAMH 34

RESULT 8
ABO77482
ID ABO77482 standard; protein; 258 AA.
XX AC ABO77482;
XX DT 29-JUL-2004 (first entry)
XX DE Pseudomonas aeruginosa polypeptide #9657.
XX KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX OS Pseudomonas aeruginosa.
XX PN US6551795-B1.
XX PD 22-APR-2003.
XX PF 18-FEB-1999; 99US-00252991.
XX PR 18-FEB-1998; 98US-0074788P.
XX PR 27-JUL-1998; 98US-0094190P.
XX PA (GENO-) GENOME THERAPEUTICS CORP.
XX PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX PI WPI; 2003-615309/58.
XX DR N-PSDB; ABD11053.
XX PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
XX PT useful as molecular targets for diagnostics, prophylaxis and treatment of
XX PT pathological conditions resulting from bacterial infection.
XX PS Disclosure; SEQ ID NO 26228; 455pp; English.
XX CC The invention relates to Pseudomonas aeruginosa polypeptides and the
XX CC polynucleotides encoding them. The sequences are useful in diagnosis and
XX CC therapy of pathological conditions, as molecular targets for diagnostics,
XX CC prophylaxis and treatment of pathological conditions resulting from a
XX CC bacterial infection, for evaluating a compound, such as a polypeptide,
XX CC for the ability to bind a *P. aeruginosa* nucleic acid, as components of
XX CC effective antibacterial targets, as targets for antibacterial drugs,
XX CC including anti-*P. aeruginosa* drugs, as templates for recombinant
XX CC production of *P. aeruginosa*-derived peptides or polypeptides, as target
XX CC components for diagnosis and/or treatment of *P. aeruginosa*-caused
XX CC infection, and in detection of *P. aeruginosa* sequences or other sequences
XX CC of Pseudomonas species using biochip technology. Sequences ABO7826-
XX CC ABO84396 represent *P. aeruginosa* polypeptides of the invention. Note: The
XX CC sequence data for this patent did not form part of the printed
XX CC specification but was obtained in electronic format from USPTO at
XX CC seqdata.uspto.gov/sequence.html
XX SQ Sequence 258 AA;

Query Match 100.0%; Score 29; DB 7; Length 258;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 278 AA;
QY 1 TYAMH 5
DB 201 TYAMH 205
RESULT 9
ID ADN27332 standard; protein; 278 AA.
XX
AC ADN27332;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #9985.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 9985; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan

Query Match 100.0%; Score 29; DB 8; Length 278;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
SQ Sequence 278 AA;
QY 1 TYAMH 5
DB 220 TYAMH 224
RESULT 10
ID AAG72483 standard; protein; 307 AA.
XX
AC AAG72483;
XX
DT 31-JUL-2001 (first entry)
XX
DE Human OR-like polypeptide query sequence, SEQ ID NO: 2164.
XX
KW Human; olfactory receptor; OR; primary scent determination;
KW secondary scent determination; polypeptide library; odour receptor;
KW scent profile; scent fingerprint; scent representation.
XX
OS Homo sapiens.
XX
PN WO200127158-A2.
XX
PD 19-APR-2001.
XX
PF 06-OCT-2000; 2000WO-US027582.
XX
PR 08-OCT-1999; 99US-0158615P.
PR 24-FEB-2000; 2000US-0184809P.
XX
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
XX WPI; 2001-290713/30.
XX
PT New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists.
XX
PS Example 6; Page 1455-1456; 1857pp; English.
XX
CC The present sequence is a polypeptide encoded by one of 344 newly mined
CC human genes. It was used as a query sequence in a database search of
CC olfactory receptor (OR)-like sequences. The invention relates to isolated
CC polynucleotides encoding polypeptides involved in olfactory sensation.
CC The polynucleotides can be used in screening for olfactory agonists and
CC antagonists. The methods allow for the determination of primary scents
CC and the identification of the odour receptors used to detect these
CC primary scents. The methods also enable determination of secondary scents
CC and the identification of combinations of odour receptors that are
CC involved in detecting such secondary scents. This enables the
CC construction of a scent representation (also called a scent fingerprint
CC or scent profile), which may be used to re-create and edit scents.
CC Libraries of olfactory receptors are useful for determining the
CC interaction pattern of a composition with the receptors, and can be used
CC for determining differences in the olfactory faculties of different
CC individuals
XX
SQ Sequence 307 AA;
QY
DB
Query Match 100.0%; Score 29; DB 4; Length 307;
Query Match

Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 154 TYAMH 158
|||||

RESULT 11
AAG71475
ID AAG71475 standard; protein; 321 AA.
XX AC AAG71475;
XX AC
XX 31-JUL-2001 (first entry)
XX Human olfactory receptor polypeptide, SEQ ID NO: 1156.
DE Human; olfactory receptor; OR; primary scent determination;
KW secondary scent determination; polypeptide library; odour receptor;
KW scent profile; scent fingerprint; scent representation.
XX Homo sapiens.
OS
XX WO200127158-A2.
XX 19-APR-2001.
XX 06-OCT-2000; 2000WO-US027582.
XX 08-OCT-1999; 99US-0158615P.
PR 24-FEB-2000; 2000US-0184809P.
XX (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
XX Bellenson J, Smith D, Lancet D, Glusman G, Fuchs T, Yanai I;
PI WPI; 2001-290713/30.
DR New polynucleotides which encode polypeptides involved in olfactory
PT sensation for identifying olfactory agonists and antagonists.
XX Claim 11; Page 674-675; 1857pp; English.

XX The present sequence is an olfactory receptor which is encoded by one of
CC a number of novel polynucleotides. The polynucleotides can be used in
CC screening for olfactory agonists and antagonists. The methods allow for
CC the determination of primary scents and the identification of the odour
CC receptors used to detect these primary scents. The methods also enable
CC determination of secondary scents and the identification of combinations
CC of odour receptors that are involved in detecting such secondary scents.
CC This enables the construction of a scent representation (also called a
CC scent fingerprint or scent profile), which may be used to re-create and
CC edit scents. Libraries of olfactory receptors are useful for determining
CC the interaction pattern of a composition with the receptors, and can be
CC used for determining differences in the olfactory faculties of different
CC individuals
XX

SQ Sequence 321 AA;
Query Match 100.0%; Score 29; DB 4; Length 321;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 169 TYAMH 173
|||||

RESULT 12
ADR10293
ID ADR10293 standard; protein; 531 AA.

XX ADR10293;
AC
XX 04-NOV-2004 (first entry)
DT Human protein useful for treating neurological disease Seq 3799.
DE human; oligo-capping method; diagnostic marker; gene therapy;
XX osteoporosis; neurological disease; Alzheimer's disease;
XX Parkinson's disease; dementia; short memory; cancer;
KW sense or motor function; emotional reaction; fear response; panic;
KW osteopathic; neuroprotective; norepinephrine; antiparkinsonian; cytostatic;
KW tranquiliser.
XX Homo sapiens.
OS
XX EPI447413-A2.
XX 18-AUG-2004.
XX 12-FEB-2004; 2004EP-00003145.
XX 14-FEB-2003; 2003JP-00102207.
PR 09-MAY-2003; 2003JP-00131452.
XX (REAS-) RES ASSOC BIOTECHNOLOGY.
XX Isogai T, Yamamoto J, Nishikawa T, Isono Y, Sugiyama T, Otsuki T;
PI Wakamatsu A, Ishii S, Nagai K, Irie R;
XX WPI; 2004-583265/57.
DR N-PSDB; ADR08337.
XX New 1995 cDNA, useful for treating osteoporosis, neurological diseases,
PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.
PS Claim 1; SEQ ID NO 3799; 2686pp; English.
XX This invention relates to novel, isolated full length human cDNA
CC molecules and the encoded proteins thereof. Specifically, it refers to
CC cDNA clones obtained by an oligo-capping method, where none of these
CC clones are identical to any known human mRNAs. The present invention
CC describes an immunoassay to identify agonists and antagonists, as well as
CC antibodies, antisense molecules and siRNAs that can all be used to bind
CC to and modulate expression of the cDNA molecules. As such, these
CC molecules are useful for diagnostic markers or therapeutic targets for
CC the various diseases or morbid states. In particular, they are useful in
CC gene therapy for treating osteoporosis, neurological disease, Alzheimer's
CC disease, Parkinson's disease, dementia, short memory and various cancers,
CC as well as for maintaining equilibrium of sense or motor function, and
CC for treating emotional reaction, fear response and panic. Accordingly,
CC they exhibit osteopathic, neuroprotective, norepinephrine, antiparkinsonian,
CC cytoskeletal and tranquiliser activities. This polypeptide is a protein
CC encoded by a full length human cDNA sequence of the invention. NOTE: This
CC sequence is not given in the sequence listing of the specification but
CC can be obtained on CD-ROM from the European Patent Office, Vienna Sub-
CC office.
XX

SQ Sequence 531 AA;
Query Match 100.0%; Score 29; DB 8; Length 531;
Best Local Similarity 100.0%; Pred. No. 3.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
Db 50 TYAMH 54
|||||

RESULT 13
RAY50844
ID RAY50844 standard; protein; 690 AA.
XX

AC	AA50844;
XX	
DT	24-FEB-2000 (first entry)
DE	
DE	A. oryzae glutaminase protein #2.
XX	
KW	Glutaminase; decomposition; glutamine; glutamic acid; ammonia;
KW	taste enhancer; seasoning; sauce; paste.
XX	
OS	Aspergillus oryzae.
XX	
FH	Key Location/Qualifiers
FT	Peptide 1..20
FT	/label= signal_peptide
FT	Protein 21..690
XX	
PN	WO9960104-A1.
XX	
PD	25-NOV-1999.
XX	
PF	12-MAY-1999; 99WO-JP002455.
XX	
PR	15-MAY-1998; 98JP-00134080.
PR	11-SEP-1998; 98JP-00258974.
PR	14-OCT-1998; 98JP-00292443.
PR	30-MAR-1999; 99JP-00089157.
XX	
PA	(AJIN) AJINOMOTO CO INC.
XX	
PI	Koibuchi K, Nagasaki H, Yuasa A, Kataoka J, Kitamoto K;
XX	
DR	WPI; 2000-053292/04.
DR	N-PSDB; AA243684.
XX	
PT	Aspergillus oryzae-originated glutaminase and partial amino-acid
PT	sequences for enhancing taste particularly in glutamic acid-converting
PT	food processing to make e.g. seasoning sauces and pastes.
XX	
PS	Example 3; Page 52-55; 74pp; Japanese.
XX	
CC	This invention describes a novel glutaminase enzyme isolated from
CC	Aspergillus oryzae which catalyses the decomposition of glutamine to
CC	glutamic acid and ammonia. The purified glutaminase and determined
CC	partial amino-acid sequence can be used for enhancing taste particularly
CC	in glutamic acid-converting food processing to give e.g. seasoning sauces
CC	and pastes as well as other seasoning materials. The gene thus obtained
CC	can be applied as probe for hybridization providing the gene-containing
CC	DNA fragments from genome and cDNA libraries of A. oryzae and A.
CC	nidulans, and subsequently modified glutaminase-producing breed. The
CC	novel strain of A. oryzae is a highly active because of its somatic
CC	secreting ability. This sequence represents the A. oryzae glutaminase
CC	enzyme described in the method of the invention
XX	
SQ	Sequence 690 AA;
	Query Match 100.0%; Score 29; DB 3; Length 690;
	Best Local Similarity 100.0%; Pred. No. 4.5e+02;
	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 TYAMH 5
Db	423 TVAMH 427
RESULT 14	
AA50835	
ID	AA50835 standard; protein; 690 AA.
XX	
AC	AA50835;
XX	
DT	24-FEB-2000 (first entry)
DE	
DE	A. oryzae glutaminase protein #1.
XX	
AC	AA50844;
XX	
DT	24-FEB-2000 (first entry)
DE	
DE	A. oryzae glutaminase protein #2.
XX	
KW	Glutaminase; decomposition; glutamine; glutamic acid; ammonia;
KW	taste enhancer; seasoning; sauce; paste.
XX	
OS	Aspergillus oryzae.
XX	
FH	Key Location/Qualifiers
FT	Peptide 1..20
FT	/label= signal_peptide
FT	Protein 21..690
XX	
PN	WO9960104-A1.
XX	
PD	25-NOV-1999.
XX	
PF	12-MAY-1999; 99WO-JP002455.
XX	
PR	15-MAY-1998; 98JP-00134080.
PR	11-SEP-1998; 98JP-00258974.
PR	14-OCT-1998; 98JP-00292443.
PR	30-MAR-1999; 99JP-00089157.
XX	
PA	(AJIN) AJINOMOTO CO INC.
XX	
PI	Koibuchi K, Nagasaki H, Yuasa A, Kataoka J, Kitamoto K;
XX	
DR	WPI; 2000-053292/04.
DR	N-PSDB; AA243684.
XX	
PT	Aspergillus oryzae-originated glutaminase and partial amino-acid
PT	sequences for enhancing taste particularly in glutamic acid-converting
PT	food processing to make e.g. seasoning sauces and pastes.
XX	
PS	Example 3; Page 52-55; 74pp; Japanese.
XX	
CC	This invention describes a novel glutaminase enzyme isolated from
CC	Aspergillus oryzae which catalyses the decomposition of glutamine to
CC	glutamic acid and ammonia. The purified glutaminase and determined
CC	partial amino-acid sequence can be used for enhancing taste particularly
CC	in glutamic acid-converting food processing to give e.g. seasoning sauces
CC	and pastes as well as other seasoning materials. The gene thus obtained
CC	can be applied as probe for hybridization providing the gene-containing
CC	DNA fragments from genome and cDNA libraries of A. oryzae and A.
CC	nidulans, and subsequently modified glutaminase-producing breed. The
CC	novel strain of A. oryzae is a highly active because of its somatic
CC	secreting ability. This sequence represents the A. oryzae glutaminase
CC	enzyme described in the method of the invention
XX	
SQ	Sequence 690 AA;
	Query Match 100.0%; Score 29; DB 3; Length 690;
	Best Local Similarity 100.0%; Pred. No. 4.5e+02;
	Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 TYAMH 5
Db	423 TVAMH 427
RESULT 15	
AA50835	
ID	AA50835 standard; protein; 703 AA.
XX	
AC	AA50835;
XX	
DT	06-DEC-2000 (first entry)
DE	
DE	Aspergillus oryzae KEN616 glutaminase.
XX	
KW	Glutaminase; Aspergillus oryzae KEN616; glutamic acid synthesis;
KW	fermentation; foodstuff production; miso; soy sauce.
XX	
OS	Aspergillus oryzae.

```
XX Key Location/Qualifiers
FH Protein 34..703
FT /note= "Mature glutaminase; specifically claimed"
XX
PN JP2000166547-A.
XX
XX 20-JUN-2000.
XX
XX 07-DEC-1998; 98JP-00347127.
XX
XX 07-DEC-1998; 98JP-00347127.
XX
XX (AICH-) AICHI KEN PREFECTURE.
XX
XX (ICHI-) ICHIBIKI KK.
XX
XX WPI; 2000-477931/42.
XX
XX N-PSDB; AAA72204.
XX
XX A new glutaminase and its preparation.
XX
XX Claim 2; Page 15-17; 27pp; Japanese.
XX
XX This sequence represents a novel glutaminase from Aspergillus oryzae
XX KBN616. The invention relates to two novel glutaminases (AAB14781,
XX AAB14782) from Aspergillus oryzae KBN616 and Aspergillus sojae BA-104
XX respectively which have molecular weights of approximately 73 kD (as
XX determined by gel filtration). The enzymes have an optimum temperature of
XX approximately 50 degrees Celsius, and an optimum pH of about 8.5. The
XX glutaminases catalyse the conversion of L-glutamine to L-glutamic acid,
XX and may be used in the production of fermented foodstuffs such as soy
XX sauce and miso
XX
XX Sequence 703 AA;
SQ
Query Match 100.0%; Score 29; DB 3; Length 703;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TYAMH 5
Db 436 TYAMH 440
```

Search completed: October 14, 2005, 16:12:37
Job time : 42.4375 secs

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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:02:59 ; Search time 6.95312 Seconds
(without alignments)
69.190 Million cell updates/sec

Title: US-10-614-959-10

Perfect score: 29

Sequence: 1 TYAMH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	122	1 M3HUGA	Ig heavy chain V-I
2	29	100.0	138	2 A35676	Ig heavy chain pre
3	29	100.0	196	2 D71184	adenylate kinase (
4	29	100.0	249	2 B32390	conserved hypothet
5	29	100.0	1151	2 H71347	hypothetical prote
6	29	100.0	1377	2 I54632	teh protein - Esch
7	26	89.7	95	2 T34500	hypothetical prote
8	26	89.7	196	2 I50675	retinol-binding pr
9	26	89.7	213	2 H86403	hypothetical prote
10	26	89.7	222	2 E90215	conserved hypothet
11	26	89.7	228	2 T22924	hypothetical prote
12	26	89.7	242	2 AD1165	B. subtilis YvpB p
13	26	89.7	242	2 AD1524	B. subtilis YvpB p
14	26	89.7	501	2 A29487	cytochrome P450 3A
15	26	89.7	501	2 A34236	cytochrome P450 3A
16	26	89.7	502	1 A34101	cytochrome P450 3A
17	26	89.7	504	2 A25222	cytochrome P450 3A
18	26	89.7	609	2 E82423	hypothetical prote
19	26	89.7	723	2 A84425	hypothetical prote
20	26	89.7	801	2 B46679	paralysed flagella
21	26	89.7	852	1 GNLJGA	pol polyprotein -
22	26	89.7	852	1 GNLJGB	pol polyprotein -
23	26	89.7	852	2 S29358	pol protein - bovi
24	26	89.7	966	2 S18955	fix23-3 protein -
25	26	89.7	1265	2 F84517	probable helicase
26	26	89.7	1385	2 T21706	hypothetical prote
27	26	89.7	1506	2 T30886	integumentary muc
28	26	89.7	6260	2 T30228	polyketide synthas
29	25	86.2	35	2 S26887	Ig heavy chain V r

RESULT 1

M3HUGA

Ig heavy chain V-III region (Ga) - human (tentative sequence)

C:Species: Homo sapiens (man)

C:Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004

C:Accession: A02052

R:Florent, G.; Lehman, D.; Putnam, F.W.

Biochemistry 13, 2482-2498, 1974

A:Title: The switch point in mu heavy chains of human IgM immunoglobulins.

A:Reference number: A02052; MUID:74175307; PMID:4208843

A:Accession: A02052

A:Molecule type: protein

A:Residues: 1-122 <FLO>

A:Cross-references: UNIPROT:P01769

C:Comment: This chain was isolated from a Waldenström's macroglobulin.

C:Genetics:

A:Gene: GDB:IGHV@

A:Cross-references: GDB:128528; OMIM:147070

A:Map position: 14q32.33-14q32.33

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin; pyroglutamic acid

F:15-98/Domain: immunoglobulin homology<IMM>

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F:22-96/Disulfide bonds: #status predicted

Query Match 100.0%; Score 29; DB 1; Length 122;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qv 1 TYAMH 5

Db 31 TYAMH 35

RESULT 2

A35676

Ig heavy chain precursor V-D-J region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 23-Jul-1999

R:White, M.B.; Word, C.J.; Humphries, C.G.; Blattner, F.R.; Tucker, P.W.

Mol. Cell. Biol. 10, 3690-3699, 1990

A:Title: Immunoglobulin D switching can occur through homologous recombination in human

A:Reference number: A35676; MUID:90287160; PMID:2113175

A:Accession: A35676

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-138 <WHI>

A:Cross-references: GB:M38066; NID:g185466; PIDN:AAA52974.1; PID:g553407

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 29; DB 2; Length 138;
 Best Local Similarity 100.0%; Pred. No. 9;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
 |||||
 Db 50 TYAMH 54

RESULT 3
 D71184
 A:Title: adenylate kinase (BC 2.7.4.3) PH1753 [similarity] - Pyrococcus horikoshii
 C:Species: Pyrococcus horikoshii
 C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
 C:Accession: D71184
 R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Seki
 M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
 DNA Res. 5, 55-76, 1998
 A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
 A:Reference number: A71000; MUID:98344137; PMID:9679194
 A:Accession: D71184
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-196 <KAW>
 A:Cross-references: UNIPROT:O59443; GB:AP0000007; NID:g3236134; PIDN:BAA30867.1; PID:g325
 A:Experimental source: strain OT3
 A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
 C:Genetics:
 A:Gene: PH1753
 C:Keywords: phosphotransferase

Query Match 100.0%; Score 29; DB 2; Length 196;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
 |||||
 Db 157 TYAMH 161

RESULT 4
 B83290
 A:Title: conserved hypothetical protein PA2847 [imported] - Pseudomonas aeruginosa (strain PA01)
 C:Species: Pseudomonas aeruginosa
 C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
 C:Accession: B83290
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bu
 adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
 ; Lory, S.; Olson, M.V.
 Nature 406, 959-964, 2000
 A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
 A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: B83290
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-249 <STO>
 A:Cross-references: UNIPROT:Q9H2Z6; GB:AE004711; GB:AE004091; NID:g9949927; PIDN:AAG0623
 A:Experimental source: strain PA01
 C:Genetics:
 A:Gene: PA2847

Query Match 100.0%; Score 29; DB 2; Length 249;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
 |||||
 Db 192 TYAMH 196

RESULT 5
 H71347

hypothetical protein TP0245 - syphilis spirochete
 C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
 C:Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 09-Jul-2004
 C:Accession: H71347
 R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin
 rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T.; McDo
 they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
 Science 281, 375-388, 1998
 A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.
 A:Reference number: A71250; MUID:98332770; PMID:9665876
 A:Accession: H71347
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-1151 <COL>
 A:Cross-references: UNIPROT:O83273; GB:AE001206; GB:AE000520; NID:g3322514; PIDN:AAC6523
 A:Experimental source: strain Nichols
 C:Genetics:
 A:Gene: TP0245
 C:Superfamily: syphilis spirochete hypothetical protein TP0245

Query Match 100.0%; Score 29; DB 2; Length 1151;
 Best Local Similarity 100.0%; Pred. No. 76;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
 |||||
 Db 700 TYAMH 704

RESULT 6
 I54632
 A:Title: tsh protein - Escherichia coli
 C:Species: Escherichia coli
 C:Date: 07-Jun-1996 #sequence_revision 07-Jun-1996 #text_change 09-Jul-2004
 C:Accession: I54632
 R:Provence, D.L.; Curtiss, R.
 Infect. Immun. 62, 1369-1380, 1994
 A:Title: Isolation and characterization of a gene involved in hemagglutination by an avi
 A:Reference number: I54632; MUID:94178945; PMID:8132344
 A:Accession: I54632
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1377 <RES>
 A:Cross-references: UNIPROT:Q47692; GB:L27423; NID:g469235; PIDN:AAA24698.1; PID:g469235
 C:Superfamily: Iga-specific metalloendopeptidase

Query Match 100.0%; Score 29; DB 2; Length 1377;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
 |||||
 Db 341 TYAMH 345

RESULT 7
 T34500
 A:Title: hypothetical protein ZK1248.17 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
 C:Accession: T34500
 R:Latreille, P.
 submitted to the EMBL Data Library, June 1995
 A:Description: The sequence of C. elegans cosmid ZK1248.
 A:Reference number: Z21534
 A:Accession: T34500
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-95 <LAT>
 A:Cross-references: UNIPROT:Q23428; EMBL:U29244; PIDN:AAC71098.1; GSPDB:GN00020; CESP:ZK
 A:Experimental source: strain Bristol N2; Clone ZK1248
 C:Genetics:
 A:Gene: CESP:ZK1248.17

A;Map position: 2
C;Superfamily: Caenorhabditis elegans major sperm protein

Query Match 89.7%; Score 26; DB 2; Length 95;
Best Local Similarity 80.0%; Pred. No. 32;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 12 TYSMH 16
|||:|

RESULT 8
I50675
retinol-binding protein precursor - chicken
C;Species: Gallus gallus (chicken)
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C;Accession: I50675; S42887
R;Vieira, A.V.; Kuchler, K.; Schneider, W.J.
DNA Cell Biol. 14, 403-410, 1995
A;Title: Retinol in avian oogenesis: molecular properties of the carrier protein.
A;Reference number: I50675; MUID:95267350; PMID:7748490
A;Accession: I50675
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-196 <VIE>
A;Cross-references: UNIPROT:P41263; EMBL:X77960; NID:g457778; PIDN:CAA54922.1; PID:g457778
C;Genetics:
A;Gene: RBP
C;Superfamily: lipocalin; lipocalin homology
F;1-21/Domain: signal sequence #status predicted <SIG>
F;36-195/Domain: lipocalin homology <LIP>
F;25-181,91-195,141-150/Disulfide bonds: #status predicted

Query Match 89.7%; Score 26; DB 2; Length 196;
Best Local Similarity 80.0%; Pred. No. 67;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 134 TYALH 138
|||:|

RESULT 9
H86403
hypothetical protein F28L5.12 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C;Accession: H86403
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
A;Accession: H86403
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-213 <STO>
A;Cross-references: UNIPROT:Q9C6N1; GB:AE051172; NID:g10998924; PIDN:AAG26064.1; GSPDB:G
C;Genetics:
A;Map position: 1

Query Match 89.7%; Score 26; DB 2; Length 213;
Best Local Similarity 80.0%; Pred. No. 73;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5

Db 202 TYALH 206
|||:|

RESULT 10
E90215
conserved hypothetical protein [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C;Accession: E90215
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
arrett, R.A.; Regan, M.A.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: E90215
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-222 <KUR>
A;Cross-references: UNIPROT:Q9UX67; GB:AE006641; NID:g13813846; PIDN:AAK40980.1; GSPDB:G
C;Genetics:
A;Gene: SSO0678
C;Superfamily: hypothetical protein MJ0570

Query Match 89.7%; Score 26; DB 2; Length 222;
Best Local Similarity 80.0%; Pred. No. 76;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 14 TYALH 18
|||:|

RESULT 11
T22924
hypothetical protein F58E6.8 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22924
R;McMurray, A.
submitted to the EMBL Data Library, April 1996
A;Reference number: Z19638
A;Accession: T22924
A;Status: preliminary; translated from GB/EMBL/DDJ
A;Molecule type: DNA
A;Residues: 1-228 <ML>
A;Cross-references: UNIPROT:Q20984; EMBL:Z70754; PIDN:CAA94778.1; GSPDB:GNO0023; CESP:F5
A;Experimental source: clone F58E6
C;Genetics:
A;Gene: CESP:F58E6.8
A;Map position: 5
A;Introns: 153/2
C;Superfamily: Caenorhabditis elegans hypothetical protein Y75B12A.2

Query Match 89.7%; Score 26; DB 2; Length 228;
Best Local Similarity 80.0%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 177 TYALH 181
|||:|

RESULT 12
AD1165
B. subtilis YvpB protein homolog lmo0724 [imported] - Listeria monocytogenes (strain EGD
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AD1165
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Faihi, H.
D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001
 A;Authors: Krefit, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
 ok, C.; Schluerter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
 A;Title: Comparative Genomics of *Listeria* species.
 A;Reference number: AB1077; MUID:21537279; PMID:11679669
 A;Accession: AD1165
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-242 <GLA>
 A;Cross-references: UNIPROT:Q8Y918; GB:NC_003210; PIDN:CAC98802.1; PID:g16410113; GSPDB:
 A;Experimental source: strain EGD-e
 C;Genetics:
 A;Gene: lmo0724
 C;Superfamily: Bacillus subtilis hypothetical protein yvpB

Query Match 89.7%; Score 26; DB 2; Length 242;
 Best Local Similarity 80.0%; Pred. No. 83;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
 |||:
 Db 191 TYSMH 195

RESULT 13
 AD1524
 B. subtilis yvpB protein homolog lin0732 [imported] - *Listeria innocua* (strain Clip11262
 C;Species: *Listeria innocua*
 C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
 C;Accession: AD1524
 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
 ; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A;Authors: Krefit, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
 ok, C.; Schluerter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
 A;Title: Comparative Genomics of *Listeria* species.
 A;Reference number: AB1077; MUID:21537279; PMID:11679669
 A;Accession: AD1524
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-242 <GLA>
 A;Cross-references: UNIPROT:Q92DT0; GB:AL592022; PIDN:CAC95964.1; PID:g16413184; GSPDB:C
 A;Experimental source: strain Clip11262
 C;Genetics:
 A;Gene: lin0732
 C;Superfamily: Bacillus subtilis hypothetical protein yvpB

Query Match 89.7%; Score 26; DB 2; Length 242;
 Best Local Similarity 80.0%; Pred. No. 83;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
 |||:
 Db 191 TYSMH 195

RESULT 14
 A29487
 Cytochrome P450 3A6 (version 1) - rabbit
 N;Alternate names: cytochrome P450 3c
 N;Contains: oxidoreductase (EC 1.-.-.-)
 C;Species: *Oryctolagus cuniculus* (domestic rabbit)
 C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
 C;Accession: A29487
 R;Dalet, C.; Clair, P.; Daujat, M.; Fort, P.; Blanchard, J.M.; Maurel, P.
 DNA 7, 39-46, 1988
 A;Title: Complete sequence of cytochrome P450 3c cDNA and presence of two mRNA species w
 A;Reference number: A29487; MUID:88166352; PMID:3349903
 A;Accession: A29487
 A;Molecule type: mRNA
 A;Residues: 1-501 <DAL>
 A;Cross-references: UNIPROT:P11707; GB:M1939; NID:g165573; PIDN:AAA31430.1; PID:g165574

C;Genetics:
 A;Gene: CYP3A6
 C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
 C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase;
 F;301-462/Domain: cytochrome P450 homology <P45>
 F;440/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 89.7%; Score 26; DB 2; Length 501;
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
 |||:
 Db 396 TYALH 400

RESULT 15
 A34236
 cytochrome P450 3A6 (version 2) - rabbit
 N;Alternate names: cytochrome P450 3c
 N;Contains: oxidoreductase (EC 1.-.-.-)
 C;Species: *Oryctolagus cuniculus* (domestic rabbit)
 C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
 C;Accession: A34236
 R;Potenza, C.L.; Pendurthi, U.R.; Strom, D.K.; Tukey, R.H.; Griffin, K.J.; Schwab, G.E.;
 J. Biol. Chem. 264, 16222-16228, 1989
 A;Title: Regulation of the rabbit cytochrome P-450 3c gene. Age-dependent expression and
 A;Reference number: A34236; MUID:89380226; PMID:2777787
 A;Accession: A34236
 A;Molecule type: mRNA
 A;Residues: 1-501 <POT>
 A;Cross-references: UNIPROT:P11707; GB:J05034; NID:g164829; PIDN:AAA31178.1; PID:g164830
 C;Genetics:
 A;Gene: CYP3A6
 C;Superfamily: human cytochrome P450 CYP3A5; cytochrome P450 homology
 C;Keywords: chromoprotein; electron transfer; heme; iron; metalloprotein; monooxygenase;
 F;300-462/Domain: cytochrome P450 homology <P45>
 F;440/Binding site: heme iron (Cys) (axial ligand) #status predicted

Query Match 89.7%; Score 26; DB 2; Length 501;
 Best Local Similarity 80.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
 |||:
 Db 396 TYALH 400

Search completed: October 14, 2005, 16:23:35
 Job time : 7.95312 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 15:51:44 ; Search time 33.2812 Seconds
(without alignments)
76.932 Million cell updates/sec

Title: US-10-614-959-10
Perfect score: 29
Sequence: 1 TYAMH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	72	2 Q8RZ81	Q8RZ81 oryza sativ
2	29	100.0	122	1 HV3H HUMAN	P01769 homo sapien
3	29	100.0	158	2 Q8PKV7	Q8PKV7 xanthomonas
4	29	100.0	196	1 KADA PYRHO	O59443 pyrococcus
5	29	100.0	249	2 Q8HZZ6	Q8HZZ6 pseudomonas
6	29	100.0	356	2 Q62C99	Q62C99 podocoryne
7	29	100.0	481	2 Q6N097	Q6N097 homo sapien
8	29	100.0	493	2 Q68CN4	Q68CN4 homo sapien
9	29	100.0	531	2 Q81WR9	Q81WR9 escherichia
10	29	100.0	544	2 Q6AQ19	Q6AQ19 desulfotale
11	29	100.0	648	2 Q9V6J4	Q9V6J4 drosophila
12	29	100.0	690	2 Q8HGS1	Q8HGS1 aspergillus
13	29	100.0	690	2 Q8UVX9	Q8UVX9 aspergillus
14	29	100.0	747	1 V222 FOWPV	Q9J513 fowlpox vir
15	29	100.0	1151	1 Y245 TREPA	Q81273 treponema p
16	29	100.0	1377	2 Q8R093	Q8R093 escherichia
17	29	100.0	1377	2 Q47692	Q47692 escherichia
18	29	100.0	7488	2 Q6JHNG	Q6JHNG saccharopol
19	26	89.7	65	2 Q62XJ3	Q62XJ3 bacillus li
20	26	89.7	95	2 Q23428	Q23428 caenorhabdi
21	26	89.7	108	2 Q6KNP8	Q6KNP8 hevea bras
22	26	89.7	138	2 Q8ZZA5	Q8ZZA5 pyrobaculum
23	26	89.7	160	2 Q7Z447	Q7Z447 homo sapien
24	26	89.7	169	2 Q66BK2	Q66BK2 yersinia ps
25	26	89.7	173	2 Q66SK1	Q66SK1 homo sapien
26	26	89.7	175	2 Q6LMV3	Q6LMV3 photobacter
27	26	89.7	187	2 Q67R88	Q67R88 symbiobacte
28	26	89.7	196	1 RETB CHICK	P41263 gallus gall
29	26	89.7	202	2 Q9CKQ5	Q9CKQ5 pasteurella
30	26	89.7	213	2 Q9C6N1	Q9C6N1 arabidopsis
31	26	89.7	217	2 Q9DG60	Q9DG60 xenopus lae

32	26	89.7	222	2 Q9UX67	Q9UX67 sulfolobus
33	26	89.7	228	2 Q20984	Q20984 caenorhabdi
34	26	89.7	229	2 Q8SHP4	Q8SHP4 trichoderma
35	26	89.7	242	2 Q8Y918	Q8Y918 listeria mo
36	26	89.7	242	2 Q92DT0	Q92DT0 listeria in
37	26	89.7	242	2 Q722H3	Q722H3 listeria mo
38	26	89.7	244	2 Q8WRC3	Q8WRC3 tetrahymena
39	26	89.7	248	2 Q88SR2	Q88SR2 pseudomonas
40	26	89.7	266	2 Q7Q8W1	Q7Q8W1 anopheles g
41	26	89.7	296	2 Q7QJUE	Q7QJUE anopheles g
42	26	89.7	302	2 Q6SM55	Q6SM55 bacillus li
43	26	89.7	304	2 Q635I5	Q635I5 bacillus ce
44	26	89.7	304	2 Q73IK1	Q73IK1 bacillus ce
45	26	89.7	304	2 Q818Z0	Q818Z0 bacillus ce

ALIGNMENTS

RESULT 1
ID Q8RZ81 PRELIMINARY; PRT; 72 AA.
AC Q8RZ81;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE B1065G12.14 protein.
GN Name=B1065G12.14;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=12447438; DOI=10.1038/nature01184;
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
Hosokawa S., Masukawa M., Arikawa K., Chiden Y., Hayashi M.,
Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
Hijishita T., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
Ikono M., Itoh S., Itoh T., Itoh Y., Iwabuchi A., Kamiya K.,
Karasawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
Machita K., Maehara T., Mizuno H., Mizubayashi T., Mukai Y.,
Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
Namiki N., Negishi M., Ohta I., Ono N., Saji S., Sakai, K., Shibata M.,
Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,
Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
Zhong H., Iwama H., Endo T., Ito H., Hann J.H., Kim H.I., Eun M.Y.,
Yano M., Jiang J., Gojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316(2002).
DR EMBL; AP003791; BAB90532.1; -
DR Gramene; Q8RZ81; -
SQ SEQUENCE 72 AA; 7677 MW; 6A9368D674BE00A3 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 72;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 25 TYAMH 29

RESULT 2
HV3H HUMAN
ID HV3H HUMAN STANDARD; PRT; 122 AA.
AC P01769;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-III region GA.

```
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=74175307; PubMed=4208843;
RA Florent G., Lehman D., Putnam P.W.;
RT "The switch point in mu heavy chains of human IgM immunoglobulins.";
RL Biochemistry 13:2482-2498(1974).
CC -!- MISCELLANEOUS: This chain was isolated from a Waldenström's
CC macroglobulin.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02052; M3HUGA.
DR HSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IgV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
KW Pyroglutamate carboxylic acid.
FT DOMAIN 1 112
FT MOD_RES 122 122 Ig-like.
FT NON_TER 122 122 Pyroglutamate carboxylic acid.
FT SEQUENCE 122 AA; 13166 MW; 745B6959E84100A CRC64;
QY Query Match 100.0%; Score 29; DB 1; Length 122;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TYAMH 5
Db 31 TYAMH 35
RESULT 3
Q8PKV7 PRELIMINARY; PRT; 158 AA.
AC Q8PKV7;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein XAC2050.
GN OrderedLocustNames=XAC2050;
OS Xanthomonas axonopodis (pv. citri).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=2022145; PubMed=12042417; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chamberg F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locati E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
```

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RL Nature 417:459-463(2002).
DR EMBL; AE011840; AAM36912.1; -.
DR InterPro; IPR001412; TRNA-synt_1.
DR PROSITE; PS00178; AA_TRNA_LIGASE_I; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 158 AA; 17289 MW; C1B1FB23AA6B930B CRC64;
QY Query Match 100.0%; Score 29; DB 2; Length 158;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TYAMH 5
Db 132 TYAMH 136
RESULT 4
KADA_PYRHO STANDARD; PRT; 196 AA.
AC O59443;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Adenylate kinase (EC 2.7.4.3) (ATP-AMP transphosphorylase).
GN Name=adkA; OrderedLocustNames=PH1753;
OS Pyrococcus horikoshii.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=53953;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=OT3;
RX MEDLINE=98344137; PubMed=9679194;
RA Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
RA Yamamoto S., Sekine M., Baba S.-I., Kosugi H., Hoshiyama A., Nagai Y.,
RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
RA Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
RA Masuchi Y., Shizuya H., Kikuchi H.;
RT "Complete sequence and gene organization of the genome of a hyper-
RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3.";
RL DNA Res. 5:55-76(1998).
CC -!- CATALYTIC ACTIVITY: ATP + AMP = 2 ADP.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the archaeal adenylate kinase family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AP000007; BAA30867.1; -.
DR PIR; D71184; D71184.
DR HSP; P43410; 1KI9.
DR HAMAP; MF_00234; -.
KW ATP-binding; Complete proteome; Kinase; Transferase.
FT NP_BIND 9 17 ATP (Potential).
SQ SEQUENCE 196 AA; 22413 MW; 26C834A1BE944D5F CRC64;
QY Query Match 100.0%; Score 29; DB 1; Length 196;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TYAMH 5
Db 157 TYAMH 161
RESULT 5
Q9H226
```

ID Q9HZZ6 PRELIMINARY; PRT; 249 AA.
 AC Q9HZZ6;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Hypothetical protein.
 GN OrderedLocustNames=PA2847;
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 15692 / PA01;
 RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
 RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
 RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
 RT opportunistic pathogen."
 RL Nature 405:959-964(2000).
 DR EMBL; AE004711; AAG06235.1; -;
 DR PIR; B83290; B83290.
 DR InterPro; IPR002781; DUF81.
 DR Pfam; PF01925; DUF81; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 249 AA; 25989 MW; 8B24827650F64D6A CRC64;

 Query Match 100.0%; Score 29; DB 2; Length 249;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 TYAMH 5
 Db 192 TYAMH 196

 RESULT 6
 Q962C9 PRELIMINARY; PRT; 356 AA.
 ID Q962C9;
 AC Q962C9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Transcription factor Cnox4-PC.
 OS Podocoryne carnea.
 OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
 OC Hydactiniidae; Podocoryne.
 OX NCBI_TaxID=6096;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21349874; PubMed=11456446; DOI=10.1006/dbio.2001.0299;
 RA Yanze N., Spring J., Schmidl C., Schmid V.;
 RT "Conservation of Hox/ParaHox-related genes in the early development of
 RT a cnidian."
 RL Dev. Biol. 236:89-98(2001).
 CC -!- SUBCELLULAR LOCATION: Nuclear (By similarity).
 DR EMBL; AY036893; AAKG3185.1; -;
 DR HSP; P09089; IK22.
 DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0003700; P:transcription factor activity; IEA.
 DR GO; GO:0006355; P:regulation of transcription, DNA-dependent; IEA.
 DR InterPro; IPR001356; Homeobox.
 DR InterPro; IPR009057; Homeodomain_like.
 DR Pfam; PF00046; Homeobox; 1.
 DR PRINTS; PR00024; HOMEBOX.
 DR PRINTS; PR00031; HTREPRESSR.
 DR SMART; SM00389; HOX; 1.
 DR PROSITE; PS00027; HOMEBOX_1; 1.

DR PROSITE; PS00071; HOMEBOX_2; 1.
 KW DNA-binding; Homeobox; Nuclear protein.
 SQ SEQUENCE 356 AA; 41170 MW; EAF5E2308D76C6BB CRC64;

 Query Match 100.0%; Score 29; DB 2; Length 356;
 Best Local Similarity 100.0%; Pred. No. 97;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 TYAMH 5
 Db 103 TYAMH 107

 RESULT 7
 Q6N097 PRELIMINARY; PRT; 481 AA.
 ID Q6N097
 AC Q6N097;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein DKFZp686H20196.
 GN Name=DKFZp686H20196;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human esophagus tumor;
 RG The German Human cDNA Consortium;
 RA Wambutt R., Heubner D., Mewes H.W., Weil B., Amid C., Osanger A.,
 RA Fobo G., Han M., Wiemann S.;
 RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BX640619; CAB45773.1; -;
 DR HSP; P01861; IADO.
 DR InterPro; IPR003599; Ig-like.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IG_C1; 3.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS00835; IG LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
 KW Hypothetical protein.
 SQ SEQUENCE 481 AA; 52759 MW; 47220D9E64BDF98B CRC64;

 Query Match 100.0%; Score 29; DB 2; Length 481;
 Best Local Similarity 100.0%; Pred. No. 1.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 TYAMH 5
 Db 50 TYAMH 54

 RESULT 8
 Q68CN4 PRELIMINARY; PRT; 493 AA.
 ID Q68CN4
 AC Q68CN4;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Hypothetical protein DKFZp686E23209 (Fragment).
 GN Name=DKFZp686E23209;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.

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RC TISUE=Rectum tumor;
RG The German cDNA Consortium;
RA Bloecker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA Osanger A., Fobo G., Han M., Wiemann S.;
RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR749861; CAH18705.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; Cl-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 493 AA; 54117 MW; A1B4F5ED3FA8AB40 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 493;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 73 TYAMH 77

RESULT 9
Q83WR9 PRELIMINARY; PRT; 531 AA.
ID Q83WR9;
AC Q83WR9;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Tsh protein (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=APC13.
RA Simoes R.C., Delicato E.R., Gaziri L.C.J., Vidotto M.C.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY280856; AAP33781.1; -.
DR GO; GO:0004252; F:serine-type endopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR000710; Peptidase S6.
DR InterPro; IPR009003; Pept_Ser_Cys.
DR Pfam; PF02395; IGAL; 1.
DR PRINTS; PR00921; IGASERPTASE.
FT NON TER 531
SQ SEQUENCE 531 AA; 56485 MW; 60AC4B859A7AFC03 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 531;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 341 TYAMH 345

RESULT 10
Q6AQ19 PRELIMINARY; PRT; 544 AA.
ID Q6AQ19;
AC Q6AQ19;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)

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DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Probable acetyl-coenzyme A synthetase.
GN Name=acs; OrderedLocusNames=Dp0825;
OS Desulfotalea psychrophila.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacterales;
OC Desulfobulbaceae; Desulfotalea.
OX NCBI_TaxID=84980;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LSv54 / DSM 12343;
RX PubMed=15305914;
RA Rabus R., Ruepp A., Frickey T., Rattei T., Fartmann B., Stark M.,
RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
RA Klenk H.-P.;
RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium
from permanently cold Arctic sediments."
RL Environ. Microbiol. 6:887-902(2004).
CC -!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
family.
DR EMBL; CR522870; CAG35554.1; -.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR000873; AMP-bind.
DR Pfam; PF00501; AMP-binding; 1.
DR PRINTS; PR00154; AMPBINDING.
DR PROSITE; PS00455; AMP_BINDING; 1.
DR Complete proteome.
KW Complete proteome.
SQ SEQUENCE 544 AA; 60412 MW; CAD62D99E4CCEBF7 CRC64;

Query Match 100.0%; Score 29; DB 2; Length 544;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 307 TYAMH 311

RESULT 11
Q9V6J4 PRELIMINARY; PRT; 648 AA.
ID Q9V6J4;
AC Q9V6J4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE CG3915-PB (GH27039p)
GN Name=Drl-2; ORFNames=CG3915;
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Megoptera; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
RA Adams M.D., Celnikier S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brannon R.C., Rogers Y.H., Blazell R.G., Chapple M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brotter P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

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RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattai B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodgett, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*;"
 RL Science 287:2185-2195(2000).
 [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celisner S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoskins R.A., Lavery T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstein G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
 melanogaster euchromatic genome sequence;"
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celisner S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 a genomics perspective;"
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P.,
 RA Bettencourt B.R., Celisner S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 systematic review;"
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 [5]
 RP SEQUENCE FROM N.A.
 RX SEQUENCE (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RG FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 [6]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA Miranda A., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA George R., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celisner S.;
 RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE003820; AAF58429.3; -;
 DR EMBL; BT004493; ARO42657.1; -;
 DR HSP; P08581; IRIW.
 DR FlyBase; FBgn0033791; Drl-2.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR001245; Tyr_kinase.
 DR InterPro; IPR008266; Tyr_kinase_AS.
 DR InterPro; IPR003306; WIF.
 DR Pfam; PF02019; WIF; 1.
 DR PRINTS; PR00109; TYRKINASE.
 DR ProDom; PD000001; Prot kinase; 1.
 DR PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PSS00103; PROTEIN_KINASE_TYR; UNKNOWN_1.
 DR PROSITE; PSS0014; WIF; 1.
 KW Kinase; Transferase; Tyrosine-protein kinase.
 SQ SEQUENCE 648 AA; 71139 MW; 1B4FAA60CB84E457 CRC64;
 Query Match 100.0%; Score 29; DB 2; Length 648;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0;
 Qy 1 TYAMH 5
 Db 56 TYAMH 60
 |||||
 |||||
 RESULT 12
 Q9HGS1 ID Q9HGS1 PRELIMINARY; PRT; 690 AA.
 AC Q9HGS1;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Glutaminase (EC 3.5.1.2).
 OS Aspergillus oryzae.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5062;
 RN [1]
 RC STRAIN=U212;
 RA Thammaraongtham C., Turner G., Moir A.J., Tanticharoen M.,
 RA Cheevadhanarak S.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY005477; AAGO2575.1; -;
 DR GO; GO:0004359; F:glutaminase activity; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 KW Hydrolase.
 SQ SEQUENCE 690 AA; 76226 MW; 6546BE2499D8D43C CRC64;
 Query Match 100.0%; Score 29; DB 2; Length 690;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 TYAMH 5
 Db 423 TYAMH 427
 |||||
 |||||
 RESULT 13
 Q9UVX9 ID Q9UVX9 PRELIMINARY; PRT; 690 AA.
 AC Q9UVX9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Glutaminase A.
 GN Name=gtAA;

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OS Aspergillus oryzae.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
OX NCBI_taxID=5062;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIB40;
RX MEDLINE=20406523; PubMed=10952006;
RA Kobuchi K., Nagasaki H., Yuasa A., Kataoka J., Kitamoto K.;
RT "Molecular cloning and characterization of a gene encoding glutaminase
from Aspergillus oryzae.";
RL Appl. Microbiol. Biotechnol. 54:59-68 (2000).
DR EMBL; AB029552; BAA86934.1; -.
SQ SEQUENCE 690 AA; 76164 MW; E3D0B17841EEA00D CRC64;

Query Match 100.0%; Score 29; DB 2; Length 690;
Best Local Similarity 100.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
DB 423 TYAMH 427

RESULT 14
V222_FOWPV
ID V222_FOWPV STANDARD; PRT; 747 AA.
AC Q9U5I3;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Putative ankryrin-repeat protein FVP222.
GN Name=FVP222;
OS Fowlpox virus (FPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Avipoxvirus.
OX NCBI_TaxID=10261;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20193820; PubMed=10729156;
RX DOI=10.1128/JVI.74.8.3815-3831.2000;
RA Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
RT "The genome of fowlpox virus.";
RL J. Virol. 74:3815-3831 (2000).
CC -!- SIMILARITY: Contains 14 ANK repeats.
CC
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CC
CC EMBL; AF198100; AAF44566.1; -.
CC HSP; O60778; IOY3.
CC InterPro; IPR002110; ANK.
CC InterPro; IPR001810; F-box.
CC Pfam; PF00023; ANK; 13.
CC Pfam; PF00646; F-box; 1.
CC PRINTS; PR01415; ANKYRIN.
CC SMART; SM00248; ANK; 15.
CC PROSITE; PS50297; ANK REP REGION; 1.
CC PROSITE; PS50088; ANK_REPEAT; 7.
KW ANK repeat; Hypothetical protein; Repeat.
FT REPEAT 38 67 ANK 1.
FT REPEAT 103 132 ANK 2.
FT REPEAT 136 165 ANK 3.
FT REPEAT 169 198 ANK 4.
FT REPEAT 202 231 ANK 5.
FT REPEAT 234 263 ANK 6.
FT REPEAT 294 323 ANK 7.
FT REPEAT 328 357 ANK 8.

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FT REPEAT 361 393 ANK 9.
FT REPEAT 397 426 ANK 10.
FT REPEAT 430 460 ANK 11.
FT REPEAT 464 493 ANK 12.
FT REPEAT 495 524 ANK 13.
FT REPEAT 529 559 ANK 14.
SQ SEQUENCE 747 AA; 85303 MW; 55F90AF2855C3D28 CRC64;

Query Match 100.0%; Score 29; DB 1; Length 747;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
DB 330 TYAMH 334

RESULT 15
Y245_TREPA
ID Y245_TREPA STANDARD; PRT; 1151 AA.
AC O83273;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Hypothetical protein TP0245.
GN OrderedLocusNames=TP0245;
OS Treponema pallidum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_taxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nichols;
RX MEDLINE=98332770; PubMed=9665876; DOI=10.1126/science.281.5375.375;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R.J., Gwin M.L., Hickey E.K., Clayton R.A., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S.L., Peterson J.D.,
RA Khalak H.G., Richardson D.L., Howell J.K., Chidambaram M.,
RA Utterback T.R., McDonald L.A., Artiach P., Bowman C., Cotton M.D.,
RA Fujii C., Garland S.A., Hatch B., Horst K., Roberts K.M., Sandusky M.,
RA Weidman J.F., Smith H.O., Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
spirochete.";
RL Science 281:375-388 (1998).
CC
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CC
CC EMBL; AF001206; AAC5239.1; -.
CC PIR; H71347; H71347.
CC TIGR; TP0245; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 1151 AA; 127556 MW; EDB63533C2CB4056 CRC64;

Query Match 100.0%; Score 29; DB 1; Length 1151;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
DB 700 TYAMH 704

Search completed: October 14, 2005, 16:19:49
Job time : 36.2812 secs

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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:00:04 ; Search time 9.84375 Seconds
(without alignments)
37.917 Million cell updates/sec

Title: US-10-614-959-10

Perfect score: 29

Sequence: 1 TYAMH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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*Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	29	100.0	118	4	US-09-232-290-45
3	29	100.0	258	4	US-09-252-991A-26228
4	29	100.0	690	4	US-10-262-083-2
5	29	100.0	690	4	US-10-262-083-18
6	26	89.7	108	4	US-09-270-767-35497
7	26	89.7	108	4	US-09-270-767-50714
8	26	89.7	454	4	US-09-489-039A-10284
9	26	89.7	455	4	US-09-543-681A-8288
10	26	89.7	502	4	US-09-949-016-5992
11	26	89.7	507	4	US-09-949-016-7091
12	26	89.7	544	4	US-09-976-594-699
13	26	89.7	544	4	US-09-919-039-270
14	25	86.2	5	1	US-08-264-093-21
15	25	86.2	5	3	US-08-918-148-26
16	25	86.2	5	4	US-09-383-667-21
17	25	86.2	5	4	US-09-138-091A-26
18	25	86.2	5	4	US-09-424-840B-34
19	25	86.2	5	4	US-09-444-840B-91
20	25	86.2	5	4	US-09-830-748B-10
21	25	86.2	38	1	US-07-977-630-67
22	25	86.2	58	4	US-09-270-767-38850
23	25	86.2	58	4	US-09-270-767-54067
24	25	86.2	98	1	US-08-211-202-118
25	25	86.2	114	4	US-09-726-219A-222
26	25	86.2	116	1	US-08-211-202-141
27	25	86.2	117	3	US-08-545-809A-91

Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 24, Appl
Sequence 145, App
Sequence 14399, A
Sequence 46, Appl
Sequence 10, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 46, Appl
Sequence 46, Appl
Sequence 45, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 13, Appl
Sequence 13, Appl
Sequence 135, App

28 25 86.2 117 3 US-09-025-769B-24
29 25 86.2 117 4 US-09-490-070A-24
30 25 86.2 117 4 US-09-490-153-24
31 25 86.2 117 4 US-09-490-324-24
32 25 86.2 118 3 US-08-545-809A-145
33 25 86.2 118 4 US-09-248-796A-14399
34 25 86.2 119 1 US-08-331-398A-46
35 25 86.2 119 2 US-08-561-521-10
36 25 86.2 119 2 US-08-561-521-12
37 25 86.2 119 2 US-08-561-521-13
38 25 86.2 119 2 US-08-331-397B-46
39 25 86.2 119 2 US-08-759-804A-46
40 25 86.2 119 3 US-09-227-693-46
41 25 86.2 119 4 US-09-438-954-41
42 25 86.2 119 5 PCT-US95-01219-10
43 25 86.2 119 5 PCT-US95-01219-12
44 25 86.2 119 5 PCT-US95-01219-13
45 25 86.2 120 1 US-08-211-202-135

ALIGNMENTS

RESULT 1
US-09-383-667-10
; Sequence 10, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Haas, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchhofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 10
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-383-667-10

Query Match 100.0%; Score 29; DB 4; Length 5;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 1 TYAMH 5

RESULT 2
US-09-232-290-45
; Sequence 45, Application US/09232290A
; Patent No. 6815540
; GENERAL INFORMATION:
; APPLICANT: PLUCKTHUN, ANDREAS
; APPLICANT: NIEBA, LARS
; APPLICANT: HONEGGER, ANNEMARIE
; TITLE OF INVENTION: IMMUNOGLOBULIN SUPER FAMILY DOMAINS AND FRAGMENTS WITH INCREASED SOLUBILITY
; FILE REFERENCE: MORPHO/7
; CURRENT APPLICATION NUMBER: US/09/232,290A
; CURRENT FILING DATE: 1999-01-15
; EARLIER APPLICATION NUMBER: PCT/EP96/02230

; EARLIER FILING DATE: 1996-05-23
; NUMBER OF SEQ ID NOS: 60
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 45
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Murine
US-09-232-290-45

Query Match 100.0%; Score 29; DB 4; Length 118;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
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|
|
Db 31 TYAMH 35

RESULT 3

US-09-252-991A-26228
; Sequence 26228, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 26228
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26228

Query Match 100.0%; Score 29; DB 4; Length 258;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
|
|
|
|
Db 201 TYAMH 205

RESULT 4

US-10-262-083-2
; Sequence 2, Application US/10262083
; Patent No. 6830905
; GENERAL INFORMATION:
; APPLICANT: KOIBUCHI, Kyoko
; APPLICANT: NAGASAKI, Hiroaki
; APPLICANT: YUASA, Ari
; APPLICANT: KATAOKA, Jiro
; APPLICANT: KITAMOTO, Katsuhiko
; TITLE OF INVENTION: A No. 6830905el Glutaminase, its Gene and a Method of Producing I
; FILE REFERENCE: 199438US-8222-10-0-PCT
; CURRENT APPLICATION NUMBER: US/10/262,083
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US/09/674,507
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: JP 10/134080
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: JP 10/258974
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: JP 10/292443
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: JP 11/89157
; PRIOR FILING DATE: 1999-03-30

; PRIOR APPLICATION NUMBER: PCT/JP99/02455
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-262-083-2

Query Match 100.0%; Score 29; DB 4; Length 690;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
|
|
|
|
Db 423 TYAMH 427

RESULT 5

US-10-262-083-18
; Sequence 18, Application US/10262083
; Patent No. 6830905
; GENERAL INFORMATION:
; APPLICANT: KOIBUCHI, Kyoko
; APPLICANT: NAGASAKI, Hiroaki
; APPLICANT: YUASA, Ari
; APPLICANT: KATAOKA, Jiro
; APPLICANT: KITAMOTO, Katsuhiko
; TITLE OF INVENTION: A No. 6830905el Glutaminase, its Gene and a Method of Producing I
; FILE REFERENCE: 199438US-8222-10-0-PCT
; CURRENT APPLICATION NUMBER: US/10/262,083
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US/09/674,507
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: JP 10/134080
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: JP 10/258974
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: JP 10/292443
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: JP 11/89157
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: PCT/JP99/02455
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-262-083-18

Query Match 100.0%; Score 29; DB 4; Length 690;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
|
|
|
|
Db 423 TYAMH 427

RESULT 6

US-09-270-767-35497
; Sequence 35497, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517

; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 35497
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-35497

Query Match 89.7%; Score 26; DB 4; Length 108;
Best Local Similarity 80.0%; Pred. No. 85;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
Db 64 TYALH 68

RESULT 7
US-09-270-767-50714
; Sequence 50714, Application US/09270767
; Patent No. 6703491
; GENERAL INFORMATION:
; APPLICANT: Homburger et al.
; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
; FILE REFERENCE: File Reference: 7326-094
; CURRENT APPLICATION NUMBER: US/09/270,767
; CURRENT FILING DATE: 1999-03-17
; NUMBER OF SEQ ID NOS: 62517
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 50714
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
; FEATURE:
; OTHER INFORMATION: Xaa means any amino acid
US-09-270-767-50714

Query Match 89.7%; Score 26; DB 4; Length 108;
Best Local Similarity 80.0%; Pred. No. 85;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
Db 64 TYALH 68

RESULT 8
US-09-489-039A-10284
; Sequence 10284, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10284
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-10284

Query Match 89.7%; Score 26; DB 4; Length 454;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:

Db 152 TYALH 156

RESULT 9

US-09-543-681A-8288
; Sequence 8288, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 8288
; LENGTH: 455
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-8288

Query Match 89.7%; Score 26; DB 4; Length 455;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
Db 225 TYALH 229

RESULT 10

US-09-949-016-5992
; Sequence 5992, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5992
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-5992

Query Match 89.7%; Score 26; DB 4; Length 502;
Best Local Similarity 80.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 TYAMH 5
|||:
Db 398 TYALH 402

RESULT 11

US-09-949-016-7091
; Sequence 7091, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

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; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7091
; LENGTH: 507
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7091
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Best Local Similarity 80.0%; Pred. No. 4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 TYAMH 5
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Db      403 TYALH 407
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RESULT 12

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US-09-976-594-699
; Sequence 699, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 699
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 4113161CD1
US-09-976-594-699
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Best Local Similarity 80.0%; Pred. No. 4.3e+02;
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Qy      1 TYAMH 5
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Db      485 TYALH 489
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RESULT 13

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US-09-919-039-270
; Sequence 270, Application US/09919039
; Patent No. 6727066
; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
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; SOFTWARE: PERL Program
; SEQ ID NO 270
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 4113161CD1
US-09-919-039-270
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Query Match      89.7%; Score 26; DB 4; Length 544;
Best Local Similarity 80.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 TYAMH 5
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Db      485 TYALH 489
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RESULT 14

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US-08-264-093-21
; Sequence 21, Application US/08264093
; Patent No. 5639863
; GENERAL INFORMATION:
; APPLICANT: Michael D. Dan
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES SPECIFIC TO
; TITLE OF INVENTION: CELL CYCLE-INDEPENDENT GLIOMA SURFACE
; TITLE OF INVENTION: ANTIGEN
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ridout & Maybee
; STREET: 2300 Richmond-Adelaide Centre
; STREET: 101 Richmond Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 2J7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.5 inch, 1.4 Mb storage
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: MS-DOS 6.00
; SOFTWARE: ASCII Editor
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/264,093
; FILING DATE:
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; CLASSIFICATION: 536
; PRIOR APPLICATION DATA: No. 5639863 applicable
; ATTORNEY/AGENT INFORMATION:
; NAME: Lake, James R.
; REGISTRATION NUMBER: 31081
; REFERENCE/DOCKET NUMBER: NOVOP/106A/7551
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 868-1482
; TELEFAX: (416) 362-0823
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; STRANDEDNESS: not applicable
; TOPOLOGY: linear
US-08-264-093-21
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Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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Db      1 SYAMH 5
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RESULT 15

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US-08-918-148-26
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; Sequence 26, Application US/08918148A
; Patent No. 6342220
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia
; APPLICANT: W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: P0979
; CURRENT APPLICATION NUMBER: US/08/918,148A
; CURRENT FILING DATE: 1997-08-25
; NUMBER OF SEQ ID NOS: 79
; SEQ ID NO 26
; LENGTH: 5
; TYPE: PRT
; ORGANISM: artificial
; FEATURE:
; NAME/KEY: 10D10scFv, 12B5scFv VH CDR1
; LOCATION: 1-5
; OTHER INFORMATION:
US-08-918-148-26
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Query Match      86.2%; Score 25; DB 3; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.1e+05;
Matches      4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 TYAMH 5
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Db      1 TYGMH 5
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:20:10 ; Search time 35.5469 Seconds
(without alignments)
58.615 Million cell updates/sec

Title: US-10-614-959-10
Perfect score: 29
Sequence: 1 TYAMH 5

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1859788

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
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4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
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6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
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8: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	29	100.0	5	18	US-10-989-462-64
2	29	100.0	11	15	US-10-468-543-91
3	29	100.0	119	20	US-11-003-819-12
4	29	100.0	121	16	US-10-466-242-25
5	29	100.0	123	18	US-10-989-462-7
6	29	100.0	128	16	US-10-466-242-47
7	29	100.0	137	16	US-10-425-115-311733
8	29	100.0	151	15	US-10-424-599-231272
9	29	100.0	158	16	US-10-425-115-211694
10	29	100.0	206	15	US-10-282-122A-52731
11	29	100.0	257	18	US-10-989-462-34
					Sequence 64, Appl
					Sequence 91, Appl
					Sequence 12, Appl
					Sequence 25, Appl
					Sequence 7, Appl
					Sequence 47, Appl
					Sequence 311733,
					Sequence 231272,
					Sequence 211694,
					Sequence 52731, A
					Sequence 34, Appl

12	29	100.0	278	15	US-10-369-493-9985	Sequence 9985, Ap
13	29	100.0	690	14	US-10-262-083-2	Sequence 2, Appl
14	29	100.0	690	14	US-10-262-083-18	Sequence 18, Appl
15	29	100.0	690	16	US-10-851-337-2	Sequence 2, Appl
16	29	100.0	690	16	US-10-851-337-18	Sequence 18, Appl
17	26	89.7	11	15	US-10-468-543-35	Sequence 35, Appl
18	26	89.7	35	16	US-10-425-113-254835	Sequence 254835,
19	26	89.7	51	16	US-10-425-113-188939	Sequence 188939,
20	26	89.7	52	16	US-10-425-113-363604	Sequence 363604,
21	26	89.7	59	15	US-10-424-599-217913	Sequence 217913,
22	26	89.7	60	15	US-10-424-599-188252	Sequence 188252,
23	26	89.7	61	16	US-10-437-963-105084	Sequence 105084,
24	26	89.7	64	16	US-10-425-115-248574	Sequence 248574,
25	26	89.7	67	9	US-09-864-761-44407	Sequence 44407, A
26	26	89.7	67	15	US-10-424-599-190876	Sequence 190876,
27	26	89.7	69	16	US-10-425-115-271914	Sequence 271914,
28	26	89.7	73	15	US-10-424-599-192746	Sequence 192746,
29	26	89.7	73	15	US-10-424-599-205833	Sequence 205833,
30	26	89.7	77	15	US-10-424-599-245586	Sequence 245586,
31	26	89.7	79	9	US-09-764-846-193	Sequence 193, App
32	26	89.7	79	14	US-10-091-483-193	Sequence 193, App
33	26	89.7	85	16	US-10-767-701-48571	Sequence 48571, A
34	26	89.7	98	15	US-10-424-599-214193	Sequence 214193,
35	26	89.7	103	16	US-10-425-115-268350	Sequence 268350,
36	26	89.7	137	15	US-10-424-599-227653	Sequence 227653,
37	26	89.7	141	15	US-10-424-599-143644	Sequence 143644,
38	26	89.7	168	16	US-10-767-701-39988	Sequence 39988, A
39	26	89.7	221	15	US-10-094-749-2980	Sequence 2980, Ap
40	26	89.7	238	10	US-09-880-748-2053	Sequence 2053, Ap
41	26	89.7	238	15	US-10-293-418-2053	Sequence 2053, Ap
42	26	89.7	304	15	US-10-282-122A-45565	Sequence 45565, A
43	26	89.7	355	17	US-10-831-070-42	Sequence 42, Appl
44	26	89.7	370	9	US-09-738-626-3768	Sequence 3768, Ap
45	26	89.7	370	9	US-09-738-626-5177	Sequence 5177, Ap

ALIGNMENTS

RESULT 1
US-10-989-462-64
; Sequence 64, Application US/10989462
; Publication No. US2005020795A1
; GENERAL INFORMATION:
; APPLICANT: Wittup, K. Dane
; APPLICANT: Yeung, Yik Andy
; TITLE OF INVENTION: ANTI-HYDROXYLASE ANTIBODIES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 01997-329001
; CURRENT FILING DATE: 2004-11-15
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US 60/520,114
; PRIOR APPLICATION NUMBER: US 60/563,514
; PRIOR FILING DATE: 2004-04-19
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 64
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-989-462-64

Query Match 100.0%; Score 29; DB 18; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5

Db 1 TYAMH 5

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RESULT 2
US-10-468-543-91
; Sequence 91, Application US/10468543
; Publication No. US20040091938A1
; GENERAL INFORMATION:
; APPLICANT: Drakenberg, Katarina
; APPLICANT: Persson, Mats
; TITLE OF INVENTION: Materials and methods for treatment of hepatitis C
; FILE REFERENCE: 0380-P03248US00
; CURRENT APPLICATION NUMBER: US/10/466,242
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/SE02/00044
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(121)
; OTHER INFORMATION: Clone 2a:14 VH
US-10-466-242-25

Query Match      100.0%; Score 29; DB 16; Length 121;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TYAMH 5
Db      33 TYAMH 37

RESULT 3
US-11-003-819-12
; Sequence 12, Application US/11003819
; Publication No. US2005015823A1
; GENERAL INFORMATION:
; APPLICANT: Evans, Elizabeth B.
; APPLICANT: Paris, Mark J.
; APPLICANT: Sahasrabudhe, Deepak M.
; APPLICANT: Zauderer, Maurice
; APPLICANT: Smith, Ernest S.
; TITLE OF INVENTION: Methods of Killing Tumor Cells by Targeting Internal Antigens
; FILE REFERENCE: 1843.0190002
; CURRENT APPLICATION NUMBER: US/11/003,819
; CURRENT FILING DATE: 2004-12-06
; PRIOR APPLICATION NUMBER: US 60/256,572
; PRIOR FILING DATE: 2003-12-04
; PRIOR APPLICATION NUMBER: US 60/531,688
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 61
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 12
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-003-819-12

Query Match      100.0%; Score 29; DB 20; Length 119;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TYAMH 5
Db      31 TYAMH 35

RESULT 4
US-10-466-242-25
; Sequence 47, Application US/10466242
; Publication No. US20040208887A1
; GENERAL INFORMATION:
; APPLICANT: Drakenberg, Katarina
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; Sequence 25, Application US/10466242
; Publication No. US20040208887A1
; GENERAL INFORMATION:
; APPLICANT: Drakenberg, Katarina
; APPLICANT: Persson, Mats
; TITLE OF INVENTION: Materials and methods for treatment of hepatitis C
; FILE REFERENCE: 0380-P03248US00
; CURRENT APPLICATION NUMBER: US/10/466,242
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/SE02/00044
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(121)
; OTHER INFORMATION: Clone 2a:14 VH
US-10-466-242-25
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Query Match      100.0%; Score 29; DB 16; Length 121;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TYAMH 5
Db      33 TYAMH 37
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RESULT 5
US-10-989-462-7
; Sequence 7, Application US/10989462
; Publication No. US20050220795A1
; GENERAL INFORMATION:
; APPLICANT: Wittrup, K. Dane
; APPLICANT: Yeung, Yik Andy
; TITLE OF INVENTION: ANTI-HYDROXYLASE ANTIBODIES AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: 01997-329001
; CURRENT APPLICATION NUMBER: US/10/989,462
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/520,114
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US 60/563,514
; PRIOR FILING DATE: 2004-04-19
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 123
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-989-462-7
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Query Match      100.0%; Score 29; DB 18; Length 123;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 TYAMH 5
Db      31 TYAMH 35
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RESULT 6
US-10-466-242-47
; Sequence 47, Application US/10466242
; Publication No. US20040208887A1
; GENERAL INFORMATION:
; APPLICANT: Drakenberg, Katarina
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; APPLICANT: Persson, Mats
; TITLE OF INVENTION: Materials and methods for treatment of hepatitis C
; FILE REFERENCE: 0380-P03248US00
; CURRENT APPLICATION NUMBER: US/10/466,242
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/SE02/00044
; PRIOR FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 47
; LENGTH: 128
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(128)
; OTHER INFORMATION: Clone 2b:5 VH
US-10-466-242-47

Query Match 100.0%; Score 29; DB 16; Length 128;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 32 TYAMH 36

RESULT 7
US-10-425-115-311733
; Sequence 311733, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 311733
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_47353C.1.pap
US-10-425-115-311733

Query Match 100.0%; Score 29; DB 16; Length 137;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 16 TYAMH 20

RESULT 8
US-10-424-599-231272
; Sequence 231272, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 231272
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(151)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_50860C.1.pap
US-10-424-599-231272

Query Match 100.0%; Score 29; DB 15; Length 151;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 120 TYAMH 124

RESULT 9
US-10-425-115-211694
; Sequence 211694, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 211694
; LENGTH: 158
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(158)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_124664C.1.pap
US-10-425-115-211694

Query Match 100.0%; Score 29; DB 16; Length 158;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 56 TYAMH 60

RESULT 10
US-10-282-122A-52731
; Sequence 52731, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant

; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELTRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52731
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Clostridium botulinum
US-10-282-122A-52731

Query Match 100.0%; Score 29; DB 15; Length 206;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 30 TYAMH 34

RESULT 11
US-10-989-462-34
; Sequence 34, Application US/10989462
; Publication No. US20050220795A1
; GENERAL INFORMATION:
; APPLICANT: Wittup, K. Dane
; APPLICANT: Yeung, Yik Andy
; TITLE OF INVENTION: ANTI-HYDROXYLASE ANTIBODIES AND USES
; FILE REFERENCE: 01997-329001
; CURRENT APPLICATION NUMBER: US/10/989,462
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/520,114
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US 60/563,514
; PRIOR FILING DATE: 2004-04-19
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: PaetSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-989-462-34

Query Match 100.0%; Score 29; DB 18; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 31 TYAMH 35

RESULT 12
US-10-369-493-9985
; Sequence 9985, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 9985
; LENGTH: 278
; TYPE: PRT
; ORGANISM: magnetite-containing magnetic coccus
US-10-369-493-9985

Query Match 100.0%; Score 29; DB 15; Length 278;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 TYAMH 5
Db 220 TYAMH 224

RESULT 13
US-10-262-083-2
; Sequence 2, Application US/10262083
; Publication No. US20030170670A1
; GENERAL INFORMATION:
; APPLICANT: KOIBUCHI, Kyoko
; APPLICANT: NAGASAKI, Hiroaki
; APPLICANT: YUASA, Ari
; APPLICANT: KATAOKA, Jiro
; APPLICANT: KITAMOTO, Katsuhiko
; TITLE OF INVENTION: A No. US20030170670A1e1 Glutaminase, its Gene and a Method of Pro
; FILE REFERENCE: 199438US-8222-10-0-PCT
; CURRENT APPLICATION NUMBER: US/10/262,083
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US/09/674,507
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: JP 10/134080
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: JP 10/258974
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: JP 10/292443
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: JP 11/89157
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: PCT/JP99/02455
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-262-083-2


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Query Match      100.0%; Score 29; DB 14; Length 690;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TYAMH 5
      |||||
Db      423 TYAMH 427

RESULT 14
US-10-262-083-18
; Sequence 18, Application US/10262083
; Publication No. US20030170670A1
; GENERAL INFORMATION:
; APPLICANT: KOIBUCHI, Kyoko
; APPLICANT: YUASA, Ari
; APPLICANT: KATAOKA, Jiro
; APPLICANT: KITAMOTO, Katsuhiko
; TITLE OF INVENTION: A NO. US20030170670A1e1 Glutaminase, its Gene and a Method of Pro
; FILE REFERENCE: 199438US-8222-10-0-PCT
; CURRENT APPLICATION NUMBER: US/10/262,083
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US/09/674,507
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: JP 10/134080
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: JP 10/258974
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: JP 10/292443
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: JP 11/89157
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: PCT/JP99/02455
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-262-083-18

Query Match      100.0%; Score 29; DB 14; Length 690;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TYAMH 5
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Db      423 TYAMH 427

RESULT 15
US-10-851-337-2
; Sequence 2, Application US/10851337
; Publication No. US20040229322A1
; GENERAL INFORMATION:
; APPLICANT: KOIBUCHI, Kyoko
; APPLICANT: NAGASAKI, Hiroaki
; APPLICANT: YUASA, Ari
; APPLICANT: KATAOKA, Jiro
; APPLICANT: KITAMOTO, Katsuhiko
; TITLE OF INVENTION: A Novel Glutaminase, its Gene and a Method of
; FILE REFERENCE: 199438US-8222-10-0-PCT
; CURRENT APPLICATION NUMBER: US/10/851,337
; CURRENT FILING DATE: 2004-05-24
; PRIOR APPLICATION NUMBER: US/10/262,083
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US/09/674,507
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: JP 10/134080
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; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: JP 10/258974
; PRIOR FILING DATE: 1998-09-11
; PRIOR APPLICATION NUMBER: JP 10/292443
; PRIOR FILING DATE: 1998-10-14
; PRIOR APPLICATION NUMBER: JP 11/89157
; PRIOR FILING DATE: 1999-03-30
; PRIOR APPLICATION NUMBER: PCT/JP99/02455
; PRIOR FILING DATE: 1999-05-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 690
; TYPE: PRT
; ORGANISM: Aspergillus oryzae
US-10-851-337-2

Query Match      100.0%; Score 29; DB 16; Length 690;
Best Local Similarity 100.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 TYAMH 5
      |||||
Db      423 TYAMH 427

Search completed: October 14, 2005, 17:00:41
Job time : 36.5469 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 15:51:19 ; Search time 130.688 Seconds
(without alignments)
50.310 Million cell updates/sec

Title: US-10-614-959-11

Perfect score: 88

Sequence: 1 IISYDGSKKYADSVKG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04.*

1: Geneseqp1980s.*

2: Geneseqp1990s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	88	100.0	17	3	AAY79069
2	87	98.9	118	5	ABB07230
3	87	98.9	248	5	ABP45312
4	87	98.9	248	5	ABP44905
5	87	98.9	248	5	ABP44903
6	87	98.9	248	7	ADG95730
7	87	98.9	248	7	ADG95732
8	87	98.9	248	7	ADG96139
9	87	98.9	251	5	ABP45103
10	87	98.9	251	7	ADG95930
11	86	97.7	135	7	ADD28319
12	85	96.6	119	5	ABB07186
13	84	95.5	117	7	ABO33850
14	84	95.5	112	7	ABO33836
15	84	95.5	119	5	ABB07169
16	84	95.5	119	8	ADI26654
17	83	94.3	17	3	AAY79076
18	83	94.3	123	8	ADP22108
19	83	94.3	125	7	ADE28443
20	83	94.3	137	7	ADD28233
21	83	94.3	137	7	ADP28321
22	83	94.3	252	5	ABP45679
23	83	94.3	252	7	ADG96506
24	83	94.3	470	7	ADE28467
25	83	94.3	614	5	ABB06275

26	82	93.2	17	2	AAW90298	Human ant
27	82	93.2	17	3	AAY79074	Anti-fact
28	82	93.2	17	3	AAY79078	Anti-fact
29	82	93.2	17	5	AAO17790	CDR2 regi
30	82	93.2	17	7	ADJ32094	Human int
31	82	93.2	17	8	ADH89402	Human tra
32	82	93.2	17	8	ADP47199	Human pho
33	82	93.2	17	8	ADS82565	Anti-IL-2
34	82	93.2	17	8	ADS52370	Fab targe
35	82	93.2	17	8	ADS52400	Fab targe
36	82	93.2	17	8	ADS52430	Fab targe
37	82	93.2	17	8	ADS52388	Fab targe
38	82	93.2	41	8	ADS84420	Human ant
39	82	93.2	41	8	ADR68562	Human EPO
40	82	93.2	61	2	AAR76975	HSV-neutr
41	82	93.2	62	2	AAR76976	HSV-neutr
42	82	93.2	66	6	ABU56837	BoNT/A HC
43	82	93.2	66	6	ABU56866	BoNT/A HC
44	82	93.2	83	2	AAW62799	Amino aci
45	82	93.2	95	3	AAB40127	Anti-hIL1

ALIGNMENTS

RESULT 1
AAY79069
ID AAY79069 standard; peptide; 17 AA.
XX
AC AAY79069;
XX
DT 12-JUN-2000 (first entry)
XX
DB Anti-factor IX/IXa antibody H chain V domain CDR2 amino acid sequence.

XX
KW Complementarity determining region 2; CDR2; antibody; Gla domain;
KW factor IX/IXa; blood coagulation; deep venous thrombosis;
KW arterial thrombosis; unstable angina; post myocardial infarction;
KW coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;
KW percutaneous transluminal coronary angioplasty; PTCA; inflammation;
KW septic shock; hypotension; adult respiratory distress syndrome; ARDS;
KW arterial fibrillation; disseminated intravascular coagulopathy; DIC.
XX
OS Homo sapiens.
XX
PN WO200012562-A1.
XX
PD 09-MAR-2000.
XX
PF 26-AUG-1999; 99WO-US019453.
XX
PR 28-AUG-1998; 98US-0098233P.
PR 03-MAR-1999; 99US-0122767P.
XX
(GETH) GENENTECH INC.
XX
PI Adams CW, Devaux B, Eaton DL, Hass PE, Judice JK, Kirchhofer D;
XX Suggett S;
XX WPI; 2000-256595/22.
XX
PT Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-carboxyglutamic acid domains useful as anti-coagulant in thrombosis, stroke, and post myocardial infarction.
XX
PS Claim 2; Fig 2; 84pp; English.

XX
CC This sequence represents a complementarity determining region 2 (CDR2) of the heavy chain variable domain of a human anti-factor IX/IXa Gla domain antibody. Factor IXa is a vitamin K dependent plasma serine protease that participates in the blood coagulation pathways. The Gla domain of factor IXa and its zymogen factor IX contains important structural determinants for interaction with high affinity binding sites on vascular endothelial

CC cells and platelets. Compositions comprising the antibodies are used for
 CC the treatment or prophylaxis of thrombotic or coagulopathic diseases or
 CC disorders in a mammal for which inhibiting a FIX/IXa mediated event is
 CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
 CC angina, post myocardial infarction, post surgical thrombosis, coronary
 CC artery bypass graft (CABG), percutaneous transluminal coronary
 CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
 CC inflammation, septic shock, hypotension, adult respiratory distress
 CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
 CC coagulopathy (DIC)

XX Sequence 17 AA;

Query Match 100.0%; Score 88; DB 3; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.2e-07; Mismatches 0; Gaps 0;
 Matches 17; Conservative 0; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKVG 17
 |||||
 Db 1 IISYDGSKKYYADSVKVG 17

RESULT 2
 ABB07230
 ID ABB07230 standard; protein; 118 AA.

XX AC ABB07230;

XX DT 26-MAR-2002 (first entry)

XX DE Anti-IL-4 receptor WAB 6-2 heavy chain variable region.

XX KW Human; antibody; interleukin; IL-4; antagonist; receptor; IL-4 receptor;
 KW antiarthritic; dermatological; antiulcer; antiinflammatory; cytostatic;
 KW antisickling; immunosuppressive; tuberculostatic; ophthalmological;
 KW antianemic; antithyroid.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Region 31..35
 /note= "complementarity determining region (CDR) 1"
 FT Region 50..66
 /note= "complementarity determining region (CDR) 2"
 FT Region 99..107
 /note= "complementarity determining region (CDR) 3"

XX WO200192340-A2.

XX PD 06-DEC-2001.

XX PF 25-MAY-2001; 2001WO-US017094.

XX PR 26-MAY-2000; 2000US-00579808.

XX PR 19-SEP-2000; 2000US-00665343.

XX PR 15-FEB-2001; 2001US-00785934.

XX PR 01-MAY-2001; 2001US-00847816.

XX PA (IMMV) IMMUNEX CORP.

XX PI Plueneke JD;

XX DR WPI; 2002-114332/15.

XX DR N-PSDB; ABA94330.

XX XX Novel human antibody which binds human interleukin (IL)-4 receptor and is
 PT capable of inhibiting IL-4 induced biological activity, functions as IL-4
 PT antagonist and is useful for treating septic arthritis, scleroderma.

XX PS Claim 4; Page 73; 85pp; English.

XX XX The invention relates to a human antibody (an interleukin (IL)-4
 CC antagonist) (I) that binds human IL-4 receptor (IL-4R), and is capable of

CC inhibiting an IL-4-induced biological activity. (I) is also useful for
 CC inhibiting both IL-4-induced biological activity and IL-13-induced
 CC biological activity in vivo in a human, and for treating septic arthritis
 CC in a human afflicted with septic arthritis. (I) is also used for treating
 CC conditions such as septic/reactive arthritis, dermatitis herpetiformis,
 CC urticaria (especially chronic idiopathic urticaria), ulcers, gastric
 CC inflammation, mucosal inflammation, ulcerative colitis, Crohn's disease,
 CC inflammatory bowel disease, other disorders of the digestive system in
 CC which IL-4 plays a role (e.g. IL-4-induced inflammation of part of the
 CC gastrointestinal tract), conditions in which IL-4-induced barrier
 CC disruption plays a role (e.g. conditions characterized by decreased
 CC epithelial barrier function in the lung or gastrointestinal tract),
 CC scleroderma, hypertrophic scarring, Whipple's disease, benign prostate
 CC hyperplasia, IL-4-induced pulmonary conditions, allergic reactions to
 CC medication, Kawasaki disease, sickle cell disease or crisis, Churg-
 CC Straus syndrome, Grave's disease, pre-eclampsia, Sjogren's syndrome,
 CC autoimmune lymphoproliferative syndrome, autoimmune haemolytic anemia,
 CC Barrett's esophagus, autoimmune uveitis, tuberculosis, nephrosis,
 CC pemphigus vulgaris or bullous pemphigoid (autoimmune blistering
 CC diseases), and myasthenia gravis (an autoimmune muscular disease). IL-4
 CC antagonists also find use as adjuvants to allergy immunotherapy and as
 CC vaccine adjuvants, especially when directing the immune response toward a
 CC TH1 response would be beneficial in treating or preventing the disease.
 CC The present sequence represents an anti-IL-4 receptor monoclonal antibody
 CC (MAb) 6-2 heavy chain variable region

XX SQ Sequence 118 AA;

Query Match 98.9%; Score 87; DB 5; Length 118;

Best Local Similarity 94.1%; Pred. No. 4.1e-06;

Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKVG 17

:|||||

Db 50 VISYDGSKKYYADSVKVG 66

RESULT 3

ID ABP45312 standard; protein; 248 AA.

XX AC ABP45312;

XX DT 19-AUG-2002 (first entry)

XX DE Human BlyS binding scFv SEQ ID 1323.

XX XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; immune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX OS Homo sapiens.

XX WO200202641-A1.

XX PD 10-JAN-2002.

XX PF 15-JUN-2001; 2001WO-US019110.

XX PR 16-JUN-2000; 2000US-0212210P.

XX PR 17-OCT-2000; 2000US-0240816P.

XX PR 16-MAR-2001; 2001US-0276248P.

XX PR 21-MAR-2001; 2001US-0277379P.

XX PR 25-MAY-2001; 2001US-0293499P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

DR WPI; 2002-114799/15.
 XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.
 XX
 XX Claim 1; Page 1981-1982; 3148pp; English.
 XX
 XX This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 XX
 XX SQ Sequence 248 AA;
 Query Match 98.9%; Score 87; DB 5; Length 248;
 Best Local Similarity 94.1%; Pred. No. 9.3e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 IISYDGSKKYYADSVKVG 17
 Db :|||||
 50 VISYDGSKKYYADSVKVG 66
 RESULT 4
 ABP44905
 ID ABP44905 standard; protein; 248 AA.
 XX
 XX AC ABP44905;
 XX
 XX DT 19-AUG-2002 (first entry)
 XX
 XX DE Human Blys binding scFv SEQ ID 916.
 XX
 XX KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 XX OS Homo sapiens.
 XX
 XX PN WO200202641-A1.
 XX
 XX PD 10-JAN-2002.
 XX
 XX PF 15-JUN-2001; 2001WO-US019110.
 XX
 XX PR 16-JUN-2000; 2000US-0212210P.
 XX PR 17-OCT-2000; 2000US-0240816P.
 XX PR 16-MAR-2001; 2001US-0276248P.
 XX PR 21-MAR-2001; 2001US-0277379P.
 XX PR 25-MAY-2001; 2001US-0293499P.
 XX
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX WPI; 2002-114799/15.
 XX

XX
 PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.
 XX
 XX Claim 1; Page 1495-1496; 3148pp; English.
 XX
 XX This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 XX
 XX SQ Sequence 248 AA;
 Query Match 98.9%; Score 87; DB 5; Length 248;
 Best Local Similarity 94.1%; Pred. No. 9.3e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 IISYDGSKKYYADSVKVG 17
 Db :|||||
 50 VISYDGSKKYYADSVKVG 66
 RESULT 5
 ABP44903
 ID ABP44903 standard; protein; 248 AA.
 XX
 XX AC ABP44903;
 XX
 XX DT 19-AUG-2002 (first entry)
 XX
 XX DE Human Blys binding scFv SEQ ID 914.
 XX
 XX KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 XX OS Homo sapiens.
 XX
 XX PN WO200202641-A1.
 XX
 XX PD 10-JAN-2002.
 XX
 XX PF 15-JUN-2001; 2001WO-US019110.
 XX
 XX PR 16-JUN-2000; 2000US-0212210P.
 XX PR 17-OCT-2000; 2000US-0240816P.
 XX PR 16-MAR-2001; 2001US-0276248P.
 XX PR 21-MAR-2001; 2001US-0277379P.
 XX PR 25-MAY-2001; 2001US-0293499P.
 XX
 XX PA (HUMA-) HUMAN GENOME SCI INC.
 XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX WPI; 2002-114799/15.
 XX

PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.

PS Claim 1; Page 1492-1493; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to
 CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention

XX SQ Sequence 248 AA;

Query Match 98.9%; Score 87; DB 5; Length 248;
 Best Local Similarity 94.1%; Pred. No. 9.3e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVK 17
 :|||||
 Db 50 VISYDGSKKYYADSVK 66

RESULT 6

ADG95730
 ID ADG95730 standard; protein; 248 AA.

XX AC ADG95730;

XX DT 11-MAR-2004 (first entry)

XX DE Single chain antibody that immunospecifically binds Blys SeqID 914.

XX KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
 KW B cell proliferation; differentiation; scFv; myasthenia gravis;
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
 KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
 KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.

XX OS Unidentified.

XX XX WO2003055979-A2.

XX PN 10-JUL-2003.

XX PD 14-NOV-2002; 2002WO-US036496.

XX PF 16-NOV-2001; 2001US-0331469P.

XX PR 19-DEC-2001; 2001US-0340817P.

XX XX (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;

XX DR WPI; 2003-505530/47.

XX PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
 PT (Blys), useful for detecting and treating diseases or disorders e.g.
 PT rheumatoid arthritis, asthma and leukemia.

XX PS Example 1; SEQ ID NO 914; 394pp; English.

XX

CC This invention relates to novel antibodies that immunospecifically bind
 CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
 CC chromosome 15q34 and encodes a protein that is a member of the tumour
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell
 CC proliferation and differentiation. Specifically, it refers to single
 CC chain antibody molecules (scFvs) derived, preferably, from the variable
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
 CC fragment thereof, of either human, murine, rat or monkey Blys. The
 CC present invention refers to the use of such antibodies in various methods
 CC for the detection, diagnosis and prognosis of diseases related to the
 CC aberrant expression or inappropriate function of Blys or its receptor. As
 CC such, these compositions are useful for identifying immune disorders
 CC including myasthenia gravis and multiple sclerosis, inflammatory
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and
 CC lymphoma. Accordingly, they can be described as exhibiting various
 CC activities such as antirheumatic, antiallergic and neuroprotective,
 CC antiinflammatory, antiasthmatic, antirheumatic and cytostatic. This
 CC polypeptide sequence is a single chain antibody that binds Blys of the
 CC invention. NOTE: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 248 AA;

Query Match 98.9%; Score 87; DB 7; Length 248;
 Best Local Similarity 94.1%; Pred. No. 9.3e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVK 17
 :|||||
 Db 50 VISYDGSKKYYADSVK 66

RESULT 7

ADG95732
 ID ADG95732 standard; protein; 248 AA.

XX AC ADG95732;

XX DT 11-MAR-2004 (first entry)

XX DE Single chain antibody that immunospecifically binds Blys SeqID 916.

XX KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
 KW B cell proliferation; differentiation; scFv; myasthenia gravis;
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
 KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
 KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.

XX OS Unidentified.

XX XX WO2003055979-A2.

XX PN 10-JUL-2003.

XX PD 14-NOV-2002; 2002WO-US036496.

XX PF 16-NOV-2001; 2001US-0331469P.

XX PR 19-DEC-2001; 2001US-0340817P.

XX XX (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;

XX DR WPI; 2003-505530/47.

XX PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
 PT (Blys), useful for detecting and treating diseases or disorders e.g.
 PT rheumatoid arthritis, asthma and leukemia.

XX PS Example 1; SEQ ID NO 916; 394pp; English.

XX

CC This invention relates to novel antibodies that immunospecifically bind
 CC to B lymphocyte stimulator (BlyS). The BlyS gene has been mapped to
 CC chromosome 13q34 and encodes a protein that is a member of the tumour
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell
 CC proliferation and differentiation. Specifically, it refers to single
 CC chain antibody molecules (scFvs) derived, preferably, from the variable
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
 CC fragment thereof, of either human, murine, rat or monkey BlyS. The
 CC present invention refers to the use of such antibodies in various methods
 CC for the detection, diagnosis and prognosis of diseases related to the
 CC aberrant expression or inappropriate function of BlyS or its receptor. As
 CC such, these compositions are useful for identifying immune disorders
 CC including myasthenia gravis and multiple sclerosis, inflammatory
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and
 CC lymphoma. Accordingly, they can be described as exhibiting various
 CC activities such as antirheumatic, antiarthritic, neuroprotective,
 CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
 CC polypeptide sequence is a single chain antibody that binds BlyS of the
 CC invention. NOTE: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published pct_sequences.
 XX
 SQ Sequence 248 AA;

Query Match 98.9%; Score 87; DB 7; Length 248;
 Best Local Similarity 94.1%; Pred. No. 9.3e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKVG 17
 :|||||
 Db 50 VISYDGSKKYYADSVKVG 66

RESULT 8
 ADG96139
 ID ADG96139 standard; protein; 248 AA.

XX AC ADG96139;

XX 11-MAR-2004 (first entry)

XX Single chain antibody that immunospecifically binds BlyS SeqID 1323.

XX antibody; B lymphocyte stimulator; BlyS; tumour necrosis factor;
 KW B cell proliferation; differentiation; scFv; myasthenia gravis;
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
 KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
 KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.

XX Unidentified.

XX WO2003055979-A2.

XX 10-JUL-2003.

XX 14-NOV-2002; 2002WO-US036496.

XX 16-NOV-2001; 2001US-0331469P.

PR 19-DEC-2001; 2001US-0340817P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;

XX WPI; 2003-505530/47.

XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator
 PT (BlyS), useful for detecting and treating diseases or disorders e.g.
 PT rheumatoid arthritis, asthma and leukemia.

XX Example 1; SEQ ID NO 1323; 394pp; English.

XX

CC This invention relates to novel antibodies that immunospecifically bind
 CC to B lymphocyte stimulator (BlyS). The BlyS gene has been mapped to
 CC chromosome 13q34 and encodes a protein that is a member of the tumour
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell
 CC proliferation and differentiation. Specifically, it refers to single
 CC chain antibody molecules (scFvs) derived, preferably, from the variable
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
 CC fragment thereof, of either human, murine, rat or monkey BlyS. The
 CC present invention refers to the use of such antibodies in various methods
 CC for the detection, diagnosis and prognosis of diseases related to the
 CC aberrant expression or inappropriate function of BlyS or its receptor. As
 CC such, these compositions are useful for identifying immune disorders
 CC including myasthenia gravis and multiple sclerosis, inflammatory
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and
 CC lymphoma. Accordingly, they can be described as exhibiting various
 CC activities such as antirheumatic, antiarthritic, neuroprotective,
 CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
 CC polypeptide sequence is a single chain antibody that binds BlyS of the
 CC invention. NOTE: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published pct_sequences.
 XX
 SQ Sequence 248 AA;

Query Match 98.9%; Score 87; DB 7; Length 248;
 Best Local Similarity 94.1%; Pred. No. 9.3e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKVG 17
 :|||||
 Db 50 VISYDGSKKYYADSVKVG 66

RESULT 9
 ABP45103

ID ABP45103 standard; protein; 251 AA.

XX AC ABP45103;

XX 19-AUG-2002 (first entry)

XX Human BlyS binding scFv SEQ ID 1114.

XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

XX WO200202641-A1.

XX 10-JAN-2002.

XX 15-JUN-2001; 2001WO-US019110.

XX 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.

XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the

PT diagnosis and treatment of cancers and immune disorders.

PS Claim 1; Page 1731-1732; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cystostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention

XX SQ Sequence 251 AA;

Query Match 98.9%; Score 87; DB 5; Length 251;
 Best Local Similarity 94.1%; Pred. No. 9.4e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKVG 17
 :|||||
 Db 50 VISYDGSKKYYADSVKVG 66

RESULT 10
 ADG95930

ID ADG95930 standard; protein; 251 AA.

XX AC ADG95930;

XX DT 11-MAR-2004 (first entry)

XX DE Single chain antibody that immunospecifically binds Blys SeqID 1114.

XX KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
 KW B cell proliferation; differentiation; scFv; myasthenia gravis;
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
 KW carcinoma; lymphoma; antirheumatic; antiallergic; neuroprotective;
 KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.

XX OS Unidentified.

XX PN WO2003055979-A2.

XX PD 10-JUL-2003.

XX PF 14-NOV-2002; 2002WO-US036496.

XX PR 16-NOV-2001; 2001US-0331469P.

XX PR 19-DEC-2001; 2001US-0340817P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;

XX WPI; 2003-505530/47.

XX DR Novel antibody that immunospecifically binds to a B lymphocyte stimulator
 PT (Blys), useful for detecting and treating diseases or disorders e.g.
 PT rheumatoid arthritis, asthma and leukemia.

XX PS Example 1; SEQ ID NO 1114; 394pp; English.

XX CC This invention relates to novel antibodies that immunospecifically bind

CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
 CC chromosome 11q34 and encodes a protein that is a member of the tumour
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell
 CC proliferation and differentiation. Specifically, it refers to single
 CC chain antibody molecules (scFvs) derived, preferably, from the variable
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
 CC fragment thereof, of either human, murine, rat or monkey Blys. The
 CC present invention refers to the use of such antibodies in various methods
 CC for the detection, diagnosis and prognosis of diseases related to the
 CC aberrant expression or inappropriate function of Blys or its receptor. As
 CC such, these compositions are useful for identifying immune disorders
 CC including myasthenia gravis and multiple sclerosis, inflammatory
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and
 CC lymphoma. Accordingly, they can be described as exhibiting various
 CC activities such as antirheumatic, antiallergic, neuroprotective,
 CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
 CC polypeptide sequence is a single chain antibody that binds Blys of the
 CC invention. NOTE: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 251 AA;

Query Match 98.9%; Score 87; DB 7; Length 251;
 Best Local Similarity 94.1%; Pred. No. 9.4e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKVG 17
 :|||||
 Db 50 VISYDGSKKYYADSVKVG 66

RESULT 11

ADD28319

ID ADD28319 standard; protein; 135 AA.

XX AC ADD28319;

XX DT 15-JAN-2004 (first entry)

XX DE Human heterodimeric antibody heavy chain variable region SEQ ID NO:97.

XX KW human heterodimeric antibody; human; antibody; binding affinity;
 KW protective antigen; Bacillus anthracis; anthrax infection; cell receptor;
 KW edema factor; lethal factor; virucide; antibacterial; immunotherapy;
 KW anti-toxin; anti-infective; anthrax; botulinum; smallpox;
 KW Venezuelan equine encephalomyelitis virus; VEEV; West Nile virus; WNV.

XX OS Synthetic.

XX OS Homo sapiens.

XX PN WO2003076568-A2.

XX PD 18-SEP-2003.

XX PF 11-FEB-2003; 2003WO-US004206.

XX PR 11-FEB-2002; 2002US-0356086P.

XX PR 29-APR-2002; 2002US-0376408P.

XX PR 27-SEP-2002; 2002US-0414053P.

XX PR 25-NOV-2002; 2002US-0428807P.

XX PA (ALEX-) ALEXION PHARM INC.

XX PI Bowdish KS, Wild MA;

XX WPI; 2003-722327/68.

XX PT New human heterodimeric antibodies or their antibody fragments, useful as
 PT anti-toxins or anti-infectives with respect to infective agents, e.g. West
 PT anthrax, botulinum, smallpox, Venezuelan equine encephalomyelitis or West
 PT Nile virus.

XX Claim 11; SEQ ID NO 97; 67pp; English.

XX The present invention describes a human heterodimeric antibody (I)

XX (fragment) having a binding affinity of at least 1x10⁻⁸ M to the

XX protective antigen of Bacillus anthracis or a molecule involved in

XX anthrax infection that blocks binding of the antigen or molecule to cell

XX receptors, edema factor and lethal factor. (I) has virucide and

XX antibacterial activities, and can be used in immunotherapy. The

XX antibodies (I) are useful as anti-toxins or anti-infectives with respect

XX to infective agents, such as anthrax, botulinum, smallpox, Venezuelan

XX equine encephalomyelitis virus (VEEV), or West Nile virus (WNV). The

XX present sequence represents a human heterodimeric antibody heavy chain

XX variable region amino acid sequence, which is used in the exemplification

XX of the present invention.

XX Sequence 135 AA;

Query Match 97.7%; Score 86; DB 7; Length 135;
 Best Local Similarity 94.1%; Pred. No. 6.8e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
 :|||||:|||||

Db 52 LISYDGSKKYYADSVKG 68

RESULT 12

ABB07186

ID ABB07186 standard; protein; 119 AA.

AC ABB07186;

XX 13-MAR-2002 (first entry)

DE shigM22 heavy chain variable region clone B sequence.

XX Neuromodulatory; central nervous system; CNS; shigM22; LYM 22; AKJR4;
 KW ebvHlgM Msl19D10; ebv HlgM CB2bG8; CB2IE12; CB2IE7; MSl19E5; virucide;
 KW antiparkinsonian; neuroprotective; nootropic; vulnerary.

XX Homo sapiens.

XX WO200185797-A1.

XX 15-NOV-2001.

XX 30-MAY-2000; 2000WO-US014902.

XX 10-MAY-2000; 2000US-00568351.

XX (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.

XX Rodriguez M, Miller DJ, Pease LR;

XX WPI; 2002-066596/09.

XX N-PSDB; ABA94243.

XX Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting

XX neurite outgrowth, regeneration, remyelination and neuroprotection in

XX central nervous system, useful to treat post-infectious

XX encephalomyelitis.

XX Claim 23; Fig 17; 219pp; English.

XX The invention provides a neuromodulatory agent (I) capable of promoting

XX neurite outgrowth, regeneration, remyelination and neuroprotection in

XX central nervous system (CNS). (I) is capable of inducing remyelination,

XX promoting cellular proliferation of glial cells, and promoting Ca²⁺

XX signaling with oligodendrocytes. An humanised antibody to (I) can be

XX selected from antibody shigM22 (LYM 22), ebvHlgM Msl19D10, ebv HlgM

XX CB2bG8, AKJR4, CB2IE12, CB2IE7 or MSl19E5. (I) is useful for stimulating

XX remyelination of CNS axons, stimulating proliferation of glial cells in

CC CNS axons, or treating demyelinating disease of CNS in a mammal in need

CC of such therapy. (I) is capable of binding to structures and cells within

CC CNS. (I) is preferably useful for treating a demyelinating disease of CNS

CC of a mouse infected with Strain DA of Theiler's murine encephalomyelitis

CC (TMEV) or for treating a human being having multiple sclerosis, or a

CC human or domestic animal with a viral demyelinating disease, or a post-

CC neural disease of CNS. (I) is also useful for an in vitro method of

CC stimulating the proliferation of glial cells from mixed cell culture. (I)

CC is also useful for stimulating remyelination of CNS axons. The antibodies

CC are useful for preventing infection by a bacterium, virus or like

CC pathogen that causes demyelination or other neurodegenerative condition

CC in a subject. Methods where (I) is administered to a patient are useful

CC for treating multiple sclerosis, Parkinson's disease, Alzheimer's

CC disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating

CC disease, CNS diseases, and other conditions in the CNS where nerves are

CC damaged as by trauma. The present sequence represents the shigM22 heavy

CC chain variable region clone B amino acid sequence

XX Sequence 119 AA;

Query Match 96.6%; Score 85; DB 5; Length 119;
 Best Local Similarity 94.1%; Pred. No. 8.6e-06;
 Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
 :|||||:|||||

Db 50 IISYDGSKKYYADSVKG 66

RESULT 13

ABO33850

ID ABO33850 standard; peptide; 17 AA.

XX ABO33850;

XX 18-SEP-2003 (first entry)

XX Anti-GPI-antibody heavy chain complementarity determining region #10.

DE Human; anti-glucose-6-phosphate isomerase-antibody; immunopolypeptide;
 KW anti-GPI-antibody; GPI; glucose-6-phosphate isomerase;
 KW autoimmune disease; rheumatoid arthritis; heavy chain variable region;
 KW VH; complementarity determining region; CDR.

XX Homo sapiens.

XX US2002146753-A1.

XX 10-OCT-2002.

XX 06-APR-2001; 2001US-00828708.

XX 06-APR-2001; 2001US-00828708.

XX (DITZ/) DITZEL H.
 (BURT/) BURTON D R.
 (SCHA/) SCHALLER M.

XX Ditzel H, Burton DR, Schaller M;

XX WPI; 2003-521517/49.

XX Immunopolypeptide for diagnosis and treatment of human autoimmune

XX disease, e.g., human rheumatoid arthritis, comprises a polypeptide that

XX binds to human glucose-6-phosphate isomerase.

XX Claim 3; Fig 4A; 47pp; English.

XX The invention describes an immunopolypeptide comprising a polypeptide

XX that binds to human glucose-6-phosphate isomerase (GPI). The methods and

XX compositions are used for diagnosis and treatment of human autoimmune

XX disease, e.g., human rheumatoid arthritis. This is the amino acid

XX sequence of human anti-GPI-antibody heavy chain variable region

```

CC complementarity determining region
XX
SQ Sequence 17 AA;

Query Match      95.5%; Score 84; DB 7; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.4e-06;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
   :|||||:|||||
Db 1 VISYDGNKKYYADSVKG 17

RESULT 14
ABO33836
ID ABO33836 standard; protein; 112 AA.
XX
AC ABO33836;
XX
DT 18-SEP-2003 (first entry)
XX
DE Human anti-GPI-antibody heavy chain variable region #3.
XX
KW Human; anti-glucose-6-phosphate isomerase-antibody; immunopolypeptide;
KW anti-GPI-antibody; GPI; glucose-6-phosphate isomerase;
KW autoimmune disease; rheumatoid arthritis; heavy chain variable region;
KW VH.
XX
OS Homo sapiens.
XX
PN US2002146753-A1.
XX
PD 10-OCT-2002.
XX
PF 06-APR-2001; 2001US-00828708.
XX
PR 06-APR-2001; 2001US-00828708.
XX
PA (DITZ/) DITZEL H.
PA (BURT/) BURTON D R.
PA (SCHA/) SCHALLER M.
XX
PI Ditzel H, Burton DR, Schaller M;
XX
DR WPI; 2003-521517/49.
XX
PT Immunopolypeptide for diagnosis and treatment of human autoimmune
PT disease, e.g., human rheumatoid arthritis, comprises a polypeptide that
PT binds to human glucose-6-phosphate isomerase.
XX
PS Claim 11; Fig 3AH; 47pp; English.
XX
CC The invention describes an immunopolypeptide comprising a polypeptide
CC that binds to human glucose-6-phosphate isomerase (GPI). The methods and
CC compositions are used for diagnosis and treatment of human autoimmune
CC disease, e.g., human rheumatoid arthritis. This is the amino acid
CC sequence of human anti-GPI-antibody heavy chain variable region
XX
SQ Sequence 112 AA;

Query Match      95.5%; Score 84; DB 7; Length 112;
Best Local Similarity 88.2%; Pred. No. 1.2e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
   :|||||:|||||
Db 43 VISYDGNKKYYADSVKG 59

RESULT 15
ABB07169
ID ABB07169 standard; protein; 119 AA.
XX
AC ABB07169;
XX
DT 13-MAR-2002 (first entry)
XX
DE sHigM22 heavy chain variable region clone A sequence.
XX
DE Neuromodulatory; central nervous system; CNS; sHigM22; LYM 22; AKJR4;
KW ebvHigM Ms119D10; ebv HigM CB2bG8; CB2iE12; CB2iE7; MS119E5; virucide;
KW antiparkinsonian; neuroprotective; neurotropic; vulneryary.
XX
KW
XX
OS Homo sapiens.
XX
PN WO200185797-A1.
XX
PD 15-NOV-2001.
XX
PF 30-MAY-2000; 2000WO-US014902.
XX
PR 10-MAY-2000; 2000US-00568351.
XX
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION RES.
XX
PI Rodriguez M, Miller DJ, Pease LR;
XX
DR WPI; 2002-066596/09.
XX
DR N-PSDB; ABA94216.
XX
PT Novel neuromodulatory agent (a human IgM monoclonal antibody), promoting
PT neurite outgrowth, regeneration, remyelination and neuroprotection in
PT central nervous system, useful to treat post-infectious
PT encephalomyelitis.
XX
PS Claim 23; Fig 17; 219pp; English.
XX
CC The invention provides a neuromodulatory agent (I) capable of promoting
CC neurite outgrowth, regeneration, remyelination and neuroprotection in
CC central nervous system (CNS). (I) is capable of inducing remyelination,
CC promoting cellular proliferation of glial cells, and promoting Ca2+
CC signaling with oligodendrocytes. An humanised antibody to (I) can be
CC selected from antibody sHigM22 (LYM 22) ebvHigM Ms119D10, ebv HigM
CC CB2bG8, AKJR4, CB2iE12, CB2iE7 or MS119E5. (I) is useful for stimulating
CC remyelination of CNS axons, stimulating proliferation of glial cells in
CC CNS axons, or treating demyelinating disease of CNS in a mammal in need
CC of such therapy. (I) is capable of binding to structures and cells within
CC CNS. (I) is preferably useful for treating a demyelinating disease of CNS
CC of a mouse infected with Strain DA of Theiler's murine encephalomyelitis
CC (TMEV) or for treating a human being having multiple sclerosis, or a
CC human or domestic animal with a viral demyelinating disease, or a post-
CC neural disease of CNS. (I) is also useful for an in vitro method of
CC stimulating the proliferation of glial cells from mixed cell culture. (I)
CC is also useful for stimulating remyelination of CNS axons. The antibodies
CC are useful for preventing infection by a bacterium, virus or like
CC pathogen that causes demyelination or other neurodegenerative condition
CC in a subject. Methods where (I) is administered to a patient are useful
CC for treating multiple sclerosis, Parkinson's disease, Alzheimer's
CC disease, amyotrophic lateral sclerosis (ALS), a viral demyelinating
CC disease, CNS diseases, and other conditions in the CNS where nerves are
CC damaged as by trauma. The present sequence represents the sHigM22 heavy
CC chain variable region clone A amino acid sequence
XX
SQ Sequence 119 AA;

Query Match      95.5%; Score 84; DB 5; Length 119;
Best Local Similarity 88.2%; Pred. No. 1.3e-05;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
   :|||||:|||||
Db 50 VISYDGNKKYYADSVKG 66

Search completed: October 14, 2005, 16:12:39
Job time : 132.688 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:02:59 ; Search time 23.6406 Seconds
(without alignments)
69.190 Million cell updates/sec

Title: US-10-614-959-11

Perfect score: 88

Sequence: 1 IISYDGSKKYYADSVKG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82	93.2	94	2	PL0120
2	82	93.2	97	2	S44115
3	82	93.2	98	2	PL0116
4	82	93.2	98	2	S29546
5	82	93.2	109	2	PH1646
6	82	93.2	109	2	PH1644
7	82	93.2	111	2	PH1643
8	82	93.2	111	2	PH1645
9	82	93.2	113	2	S38490
10	82	93.2	114	2	S46390
11	82	93.2	114	2	S46392
12	82	93.2	117	2	S36270
13	82	93.2	118	2	S31677
14	82	93.2	118	2	S31116
15	82	93.2	119	2	P36005
16	82	93.2	120	2	S31112
17	82	93.2	121	2	S19666
18	82	93.2	121	2	G36005
19	82	93.2	122	2	E36005
20	82	93.2	122	2	S31119
21	82	93.2	123	2	S38493
22	82	93.2	130	2	PL0098
23	82	93.2	132	2	S31603
24	82	93.2	134	2	S31679
25	82	93.2	139	2	S31674
26	77	87.5	137	2	S31701
27	75	85.2	108	2	PH1642
28	75	85.2	114	2	S46391
29	75	85.2	119	2	S31111

ALIGNMENTS

RESULT 1

PL0120

Ig heavy chain V-III region (TD-Vo) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jul-2004

C;Accession: PL0120

R;Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.

J. Exp. Med. 168, 229-245, 1988

A;Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin

A;Reference number: PL0116; MUID:88286083; PMID:2840480

A;Accession: PL0120

A;Molecule type: mRNA

A;Residues: 1-94 <BIR>

A;Cross-references: UNIPROT:Q8MUK1; UNIPROT:Q9UL93

A;Experimental source: B cells from patient TD with acute lymphoblastic leukemia, ALL

A;Note: the sequence shows the V region (TD-Vo) from a nonproductive DNA rearrangement

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin

F;31-35/Region: complementarity-determining 1

F;49-65/Region: complementarity-determining 2

Query Match 93.2%; Score 82; DB 2; Length 94;

Best Local Similarity 88.2%; Pred. No. 7.2e-06;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17

Db 50 VISYDGSNKYYADSVKG 66

RESULT 2

S44115

Ig heavy chain V region - human

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001

C;Accession: S44115

R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.

submitted to the EMBL Data Library, March 1994

A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r

A;Reference number: S44105

A;Accession: S44115

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-97 <HAW>

A;Cross-references: EMBL:Z11384; NID:g472969; PIDN:CA83259.1; PID:g940526

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 93.2%; Score 82; DB 2; Length 97;

Best Local Similarity 88.2%; Pred. No. 7.5e-06;

Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:||||| |||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 3

PL0116
Ig heavy chain V-III region (AW-Vx) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 23-Jul-1999
C:Accession: PL0116; S26892
R:Bird, J.; Galili, N.; Link, M.; Stites, D.; Sklar, J.
J. Exp. Med. 168, 229-245, 1988
A:Title: Continuing rearrangement but absence of somatic hypermutation in immunoglobulin A.
A:Reference number: PL0116; MUID:88286083; PMID:2840480
A:Accession: PL0116
A:Molecule type: mRNA
A:Residues: 1-98 <BIR>
A:Experimental source: B cells from patient AW with acute lymphoblastic leukemia, ALL
A>Note: the sequence shows the V region (AW-Vx) from a nonproductive DNA rearrangement f
R:Tonlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26892
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z12349; NID:g32918; PIDN:CAA78219.1; PID:g32919
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: acute lymphoblastic leukemia; heterotetramer; immunoglobulin
P:15-98/Domain: immunoglobulin homology <IMM>
F:31-35/Region: complementarity-determining 1
F:49-65/Region: complementarity-determining 2

Query Match 93.2%; Score 82; DB 2; Length 98;
Best Local Similarity 88.2%; Pred. No. 7.5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:||||| |||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 4

S29546
Ig heavy chain V region (COS-8 / DP-46) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 07-Jan-1994 #sequence_revision 17-Nov-1995 #text_change 23-Jul-1999
C:Accession: S29546; S26888
R:Tonlinson, M.; Walter, G.; Cook, G.P.; Winter, G.
submitted to the EMBL Data Library, October 1992
A:Reference number: S29543
A:Accession: S29546
A:Molecule type: DNA
A:Residues: 1-98 <TOM>
A:Cross-references: EMBL:Z17394; NID:g32843; PIDN:CAA78997.1; PID:g32844
A>Note: designated COS-8
R:Tonlinson, I.M.; Walter, G.; Marks, J.D.; Llewelyn, M.B.; Winter, G.
J. Mol. Biol. 227, 776-798, 1992
A:Title: The repertoire of human germline V(H) sequences reveals about fifty groups of V
A:Reference number: S26885; MUID:93021117; PMID:1404388
A:Accession: S26888
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <TO2>
A:Cross-references: EMBL:Z12346; NID:g32912; PIDN:CAA78216.1; PID:g32913
A>Note: designated DP-46
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 98;

Best Local Similarity 88.2%; Pred. No. 7.5e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Qy 1 IISYDGSKKYYADSVKG 17
:||||| |||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 5

PH1646
Ig heavy chain V region (clone 6H12) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C:Accession: PH1646
R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo
A:Reference number: PH1642; MUID:93301610; PMID:8315388
A:Accession: PH1646
A:Molecule type: mRNA
A:Residues: 1-109 <HIL>
A:Cross-references: UNIPROT:Q8WUK1
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 109;
Best Local Similarity 88.2%; Pred. No. 8.4e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:||||| |||
Db 42 VISYDGSNKYYADSVKG 58

RESULT 6

PH1644
Ig heavy chain V region (clone 5D11) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C:Accession: PH1644
R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo
A:Reference number: PH1642; MUID:93301610; PMID:8315388
A:Accession: PH1644
A:Molecule type: mRNA
A:Residues: 1-109 <HIL>
A:Cross-references: UNIPROT:Q9UL93
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:7-90/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 109;
Best Local Similarity 88.2%; Pred. No. 8.4e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:||||| |||
Db 42 VISYDGSNKYYADSVKG 58

RESULT 7

PH1643
Ig heavy chain V region (clone 6H7) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C:Accession: PH1643
R:Hillson, J.L.; Karr, N.S.; Opplinger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A:Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylo
A:Reference number: PH1642; MUID:93301610; PMID:8315388
A:Accession: PH1643

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A;Molecule type: mRNA
A;Residues: 1-111 <HIL>
A;Cross-references: UNIPROT:Q8WUK1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match      93.2%; Score 82; DB 2; Length 111;
Best Local Similarity 88.2%; Pred. No. 8.6e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 IISYDGSKKYYADSVK 17
Db      42 VISYDGSNKYYADSVK 58

RESULT 8
PH1645
Ig heavy chain V region (clone 6C8) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C;Accession: PH1645
R;Hillson, J.L.; Karr, N.S.; Oppliger, I.R.; Mannik, M.; Sasso, E.H.
J. Exp. Med. 178, 331-336, 1993
A;Title: The structural basis of germline-encoded VH3 immunoglobulin binding to staphylococcal protein A
A;Reference number: PH1642; MUID:93301610; PMID:8315388
A;Accession: PH1645
A;Molecule type: mRNA
A;Residues: 1-111 <HIL>
A;Cross-references: UNIPROT:Q8WUK1
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;7-90/Domain: immunoglobulin homology <IMM>

Query Match      93.2%; Score 82; DB 2; Length 111;
Best Local Similarity 88.2%; Pred. No. 8.6e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 IISYDGSKKYYADSVK 17
Db      42 VISYDGSNKYYADSVK 58

RESULT 9
S38490
Ig heavy chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C;Accession: S38490
R;Marks, J.D.; Owehand, W.H.; Bye, J.M.; Finnern, R.; Gorick, B.D.; Voak, D.; Thorpe, S.
submitted to the EMBL Data Library, June 1993
A;Description: Human antibody fragments specific for human blood group antigens from a phage display library
A;Reference number: S38488
A;Accession: S38490
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-113 <MAR>
A;Cross-references: EMBL:Z23030; NID:g414027; PIDN:CAA80565.1; PID:g414028
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match      93.2%; Score 82; DB 2; Length 113;
Best Local Similarity 88.2%; Pred. No. 8.7e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 IISYDGSKKYYADSVK 17
Db      50 VISYDGSNKYYADSVK 66

RESULT 10
S46390
Ig heavy chain V region - human
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: S46390
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by phage display
A;Reference number: S46390; MUID:94254092; PMID:8196048
A;Accession: S46390
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-114 <FIG>
A;Cross-references: EMBL:Z31686; NID:g509782; PIDN:CAA83491.1; PID:g1335143
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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```
Query Match      93.2%; Score 82; DB 2; Length 114;
Best Local Similarity 88.2%; Pred. No. 8.8e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 IISYDGSKKYYADSVK 17
Db      50 VISYDGSNKYYADSVK 66

RESULT 11
S46392
Ig heavy chain V region (VH-28) - human
C;Species: Homo sapiens (man)
C;Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 20-Jun-2000
C;Accession: S46392
R;Figini, M.; Marks, J.D.; Winter, G.; Griffiths, A.D.
J. Mol. Biol. 239, 68-78, 1994
A;Title: In vitro assembly of repertoires of antibody chains on the surface of phage by phage display
A;Reference number: S46390; MUID:94254092; PMID:8196048
A;Accession: S46392
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-114 <FIG>
A;Cross-references: EMBL:Z31688; NID:g499306; PIDN:CAA83493.1; PID:g1335145
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match      93.2%; Score 82; DB 2; Length 114;
Best Local Similarity 88.2%; Pred. No. 8.8e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 IISYDGSKKYYADSVK 17
Db      50 VISYDGSNKYYADSVK 66

RESULT 12
S36270
Ig heavy chain V region (clone alpha-TNF-E1) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Jul-1999
C;Accession: S36270
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36270
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-117 <GRI>
A;Cross-references: EMBL:Z18839; NID:g33118; PIDN:CAA79291.1; PID:g939898
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>
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Query Match 93.2%; Score 82; DB 2; Length 117;
 Best Local Similarity 88.2%; Pred. No. 9e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
 :||||| |||||
 Db 50 VISYDGSNKYYADSVKG 66

RESULT 13

S31677
 Ig heavy chain V region - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
 C:Accession: S31677
 R:Cuisinier, A.M.; Gauthier, L.; Boubli, L.; Pougereau, M.; Tonnelle, C.
 submitted to the EMBL Data Library, June 1992
 A:Description: Mechanisms that generate human immunoglobulin diversity operate from the
 A:Reference number: S31585
 A:Accession: S31677
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-118 <CUI>
 A:Cross-references: EMBL:Z14172; NID:G31009; PIDN:CAA78541.1; PID:G31010
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin

Query Match 93.2%; Score 82; DB 2; Length 118;
 Best Local Similarity 88.2%; Pred. No. 9.1e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
 :||||| |||||
 Db 50 VISYDGSNKYYADSVKG 66

RESULT 14

S31116
 Ig heavy chain - human
 C:Species: Homo sapiens (man)
 C>Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
 C:Accession: S31116
 R:Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman
 Eur. J. Immunol. 22, 247-251, 1992
 A>Title: Restricted utilization of germ-line V(H)3 genes and short diverse third complement
 A:Reference number: S31104; MUID:92111633; PMID:1730252
 A:Accession: S31116
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: mRNA
 A:Residues: 1-118 <RAA>
 A:Cross-references: UNIPROT:Q8WUK1; EMBL:X62966
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 118;
 Best Local Similarity 88.2%; Pred. No. 9.1e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
 :||||| |||||
 Db 50 VISYDGSNKYYADSVKG 66

RESULT 15

F36005
 Ig heavy chain V region (M49) - human
 C:Species: Homo sapiens (man)
 C>Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 09-Jul-2004
 C:Accession: F36005
 R:Schroeder Jr., H.W.; Wang, J.Y.
 Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990

A>Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
 A:Reference number: A36005; MUID:90349571; PMID:2117273
 A:Accession: F36005
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-119 <SCH>
 A:Cross-references: UNIPROT:Q8WUK1; GB:M34026
 C:Genetics:
 A:Gene: GDB:IGH@; IGHDI1
 A:Cross-references: GDB:118731; OMIM:146910
 A:Map position: 14q32.33-14q32.33
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotetramer; immunoglobulin
 F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 93.2%; Score 82; DB 2; Length 119;
 Best Local Similarity 88.2%; Pred. No. 9.2e-06;
 Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
 :||||| |||||
 Db 50 VISYDGSNKYYADSVKG 66

Search completed: October 14, 2005, 16:23:36
 Job time : 24.6406 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 15:51:44 ; Search time 113.156 Seconds
(without alignments)
76.932 Million cell updates/sec

Title: US-10-614-959-11
Perfect score: 88
Sequence: 1 IISYDGSKKYYADSVKG 17

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	82	93.2	116	2 Q9UL93	Q9ul93 homo sapien
2	82	93.2	240	2 Q65ZC9	Q65zc9 homo sapien
3	82	93.2	613	2 Q8WUK1	Q8wuk1 homo sapien
4	74	84.1	113	2 Q8UL90	Q8ul90 homo sapien
5	74	84.1	122	1 HV3G_HUMAN	P01768 homo sapien
6	71	80.7	417	2 Q6N093	Q6n093 homo sapien
7	70	79.5	493	2 Q68CN4	Q68cn4 homo sapien
8	69	78.4	147	2 Q9Y509	Q9y509 homo sapien
9	67	76.1	482	2 Q7Z351	Q7z351 homo sapien
10	67	76.1	493	2 Q8NCL6	Q8ncl6 homo sapien
11	66	75.0	122	2 Q9UL84	Q9ul84 homo sapien
12	65	73.9	119	1 HV3L_HUMAN	P01773 homo sapien
13	64	72.7	95	2 Q9ULB6	Q9ulb6 homo sapien
14	64	72.7	122	1 HV3H_HUMAN	P01769 homo sapien
15	64	72.7	470	2 Q6PJ44	Q6pja4 homo sapien
16	64	72.7	478	2 Q6PI81	Q6pi81 homo sapien
17	63	71.6	119	1 HV3I_HUMAN	P01770 homo sapien
18	63	71.6	614	2 Q6DDQ7	Q6ddq7 xenopus lae
19	62	70.5	121	1 HV3J_HUMAN	P01771 homo sapien
20	62	70.5	519	2 Q6N092	Q6n092 homo sapien
21	61	69.3	121	2 Q9UL71	Q9ul71 homo sapien
22	61	69.3	544	2 Q6PJ95	Q6pi95 homo sapien
23	60	68.2	118	2 Q9UL72	Q9ul72 homo sapien
24	56	63.6	116	1 HV05_CARAU	P19181 carassius a
25	56	63.6	126	1 HV3K_HUMAN	P01772 homo sapien
26	56	63.6	593	2 Q6INM5	Q6inm5 xenopus lae
27	55	62.5	481	2 Q6N097	Q6n097 homo sapien
28	53	60.2	464	2 Q6MZU6	Q6mzu6 homo sapien
29	53	60.2	597	2 Q96BB9	Q96bb9 homo sapien
30	52.5	59.7	122	1 HV3A_HUMAN	P01762 homo sapien
31	52	59.1	115	1 HV3F_HUMAN	P01767 homo sapien

32	52	59.1	456	2 Q6IN78	Q6in78 homo sapien
33	52	59.1	475	2 Q6MZQ6	Q6mzq6 homo sapien
34	52	59.1	493	2 Q6GMX2	Q6gmx2 homo sapien
35	50	56.8	114	1 HV3B_HUMAN	P01763 homo sapien
36	50	56.8	119	2 Q920E7	Q920e7 mus musculu
37	50	56.8	136	2 Q65ZL8	Q65zl8 mus musculu
38	50	56.8	585	2 Q6GXA4	Q6gpx4 xenopus lae
39	49	55.7	71	2 Q9GJ71	Q9gj71 salmo trutt
40	49	55.7	87	2 Q9AV03	Q9av03 oryza sativ
41	49	55.7	98	1 HV57_MOUSE	P18528 mus musculu
42	49	55.7	117	1 HV3C_HUMAN	P01764 homo sapien
43	49	55.7	480	2 Q6N094	Q6n094 homo sapien
44	49	55.7	1048	1 YC8I_METJA	Q58677 methanococc
45	48.5	55.1	247	2 Q9VZF9	Q9vzf9 drosophila

ALIGNMENTS

RESULT 1
Q9UL93 ID Q9UL93 PRELIMINARY; PRT; 116 AA.
AC Q9UL93;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region (Fragment).
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M., Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal fetus."
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035021; AAD56257.1; -.
DR PIR; P01644; PHL644.
DR PIR; P0120; PLO120.
DR HSSP; P01772; 2FBA.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 116
SQ SEQUENCE 116 AA; 12434 MW; 0DA0348154DD6061 CRC64;

Query Match 93.2%; Score 82; DB 2; Length 116;
Best Local Similarity 88.2%; Pred. No. 1e-05; 1; Indels 0; Gaps 0;
Matches 15; Conservative 1; Mismatches 1;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 49 VISYDGSNKYYADSVKG 65

RESULT 2
Q65ZC9 ID Q65ZC9 PRELIMINARY; PRT; 240 AA.
AC Q65ZC9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Single-chain Fv (Fragment).
DE Name=scFv;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C1q/7;
RX MEDLINE=97362799; PubMed=9219263;
RA Kontermann R.E., Wing M.G., Winter G.;
RT "Complement recruitment using bispecific diabodies.";
RL Nat. Biotechnol. 15:629-631(1997).
DR EMBL; Y13056; CAA73499.1; -.
DR InterPro; IPR003599; IG-.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 2.
DR PROSITE; PS50835; IG_LIKE; 2.
FT NON TER 1
FT NON TER 240
SQ SEQUENCE 240 AA; 25569 MW; FDCFD3645F64B373 CRC64;

Query Match 93.2%; Score 82; DB 2; Length 240;
Best Local Similarity 88.2%; Pred. No. 2.3e-05;
Matches 15; Conservative 1; Mismatches 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
Db 50 VISYDGSNKYYADSVKG 66

RESULT 3
Q8WU1 PRELIMINARY; PRT; 613 AA.
AC Q8WU1;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHM protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=23288257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska J., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC020240; AAH20240.1; -.
DR PIR; F36005; F36005.
DR PIR; G36005; G36005.
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DR PIR; PH1642; PH1642.
DR PIR; PH1643; PH1643.
DR PIR; PH1645; PH1645.
DR PIR; PH1646; PH1646.
DR PIR; PL0098; PL0098.
DR PIR; PL0120; PL0120.
DR PIR; S15590; S15590.
DR PIR; S31116; S31116.
DR PIR; S31119; S31119.
DR PIR; S70442; S70442.
DR HSSP; P01861; IADQ.
DR Pfam; PF07654; C1-set; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 3.
SQ SEQUENCE 613 AA; 67295 MW; 60C7F5950671E315 CRC64;

Query Match 93.2%; Score 82; DB 2; Length 613;
Best Local Similarity 88.2%; Pred. No. 6.4e-05;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
Db 69 VISYDGSNKYYADSVKG 85

RESULT 4
Q9UL90 PRELIMINARY; PRT; 113 AA.
AC Q9UL90;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/clin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035024; AAD56260.1; -.
DR PIR; S78486; S78486.
DR HSSP; P01772; 2FB4.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 113
SQ SEQUENCE 113 AA; 12437 MW; ED57PDD19086D07F CRC64;

Query Match 84.1%; Score 74; DB 2; Length 113;
Best Local Similarity 87.5%; Pred. No. 0.00022;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 ISYDGSKKYYADSVKG 17
Db 51 IRYDGSNKYYADSVKG 66

RESULT 5
HV3G HUMAN
ID HV3G HUMAN STANDARD; PRT; 122 AA.
AC P01768;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
```

DR	PROSITE; PS50835; IG_LIKE; 3.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW	Hypothetical protein.
FT	NON_TER 1
SQ	SEQUENCE 417 AA; 46061 MW; C4518E844CFB883C CRC64;
 Query Match 80.7%; Score 71; DB 2; Length 417; Best Local Similarity 70.6%; Pred. No. 0.0029; Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;	
QY	1 IISYDGSKKYYADSVKG 17 :- : :-
Db	22 VIAYDSTQYYADSVRG 38 :- : :-
 RESULT 7	
Q68CN4	PRELIMINARY; PRT; 493 AA.
ID	Q68CN4
AC	Q68CN4
DT	23-OCT-2004 (TrEMBLrel. 28, Created)
DT	25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT	25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE	Hypothetical protein DKFZp686E23209 (Fragment).
GN	Name=DKFZp686E23209;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCB1_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Rectum tumor;
RG	The German cDNA Consortium;
RA	Bloeker H., Boecher M., Brandt P., Mewes H.W., Weil B., Amid C.,
RA	Ossinger A., Fobo G., Han M., Wiemann S.;
RL	Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
DR	EMBL; CR749861; CAH18705.1; -
DR	InterPro; IPR003599; Ig.
DR	InterPro; IPR007110; Ig-like.
DR	InterPro; IPR003597; Ig cl.
DR	InterPro; IPR003006; Ig_MHC.
DR	InterPro; IPR003596; Ig_v.
DR	Pfam; PF07654; Cl-set; 3.
DR	Pfam; PF00047; Ig; 4.
DR	SMART; SM00409; IG; 2.
DR	SMART; SM00407; IGcl; 3.
DR	SMART; SM00406; IGV; 1.
DR	PROSITE; PS50835; IG_LIKE; 4.
DR	PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW	Hypothetical protein.
FT	NON_TER 1
SQ	SEQUENCE 493 AA; 54117 MW; A1E4F5ED3FA8AB40 CRC64;
 Query Match 79.5%; Score 70; DB 2; Length 493; Best Local Similarity 70.6%; Pred. No. 0.0052; Matches 12; Conservative 4; Mismatches 1; Indels 0; Gaps 0;	
QY	1 IISYDGSKKYYADSVKG 17 :- : :-
Db	92 VISEGKGHYADSVKG 108 :- : :-
 RESULT 8	
Q9Y509	PRELIMINARY; PRT; 147 AA.
ID	Q9Y509
AC	Q9Y509
DT	01-NOV-1999 (TrEMBLrel. 12, Created)
DT	01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	VH3 protein (Fragment).
GN	Name=VH3;
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96071149; PubMed=7475288;
RA Cao J., Vescio R.A., Rettig M.B., Hong C.H., Kim A., Lee J.C.,
RA Lichtenstein A.K., Berenson J.R.;
RT "A CD10-positive subset of malignant cells is identified in multiple
RT myeloma using PCR with patient-specific immunoglobulin gene primers.";
RL Leukemia 9:1948-1953(1995).
DR EMBL; S80860; AADI4339.1; -.
DR HSSP; P01842; IAQK.
DR GO; GO:0005887; C: integral to plasma membrane; NAS.
DR GO; GO:0016066; P: cellular defense response (sensu Vertebrata); NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 147
SQ SEQUENCE 147 AA; 15768 MW; 8489FCAA7BC925C CRC64;

Query Match 78.4%; Score 69; DB 2; Length 147;
Best Local Similarity 76.5%; Pred. No. 0.002;
Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||:|||||
Db 50 LISYDGSQYYAGSVKG 66

RESULT 9
QY 072351 PRELIMINARY; PRT; 482 AA.
AC Q72351;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein DKFZp686N02209.
GN Name=DKFZp686N02209;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Human rectum tumor;
RA Bloeker H., Boecker H., Mewes H.W., Well B., Amid C., Osanger A.,
RA Fobo G., Han M., Wiemann S.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BX538118; CAD98026.1; -.
DR HSSP; P01857; 1H2H.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 482 AA; 52852 MW; ED475F1901D1A034 CRC64;

Query Match 76.1%; Score 67; DB 2; Length 482;
Best Local Similarity 70.6%; Pred. No. 0.016;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||:|||||
Db 69 VISYDGNHLYSDSVKG 85

RESULT 10
QY 08NCL6 PRELIMINARY; PRT; 493 AA.
ID Q8NCL6

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AC Q8NCL6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein FLJ90170.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Mammary gland;
RA Isogai T., Ota T., Nishikawa T., Hayashi K., Otsuki T., Sugiyama T.,
RA Suzuki Y., Nagai K., Sugano S., Ishii S., Kawai-Hio Y., Saito K.,
RA Yamamoto J., Wakamatsu A., Nakamura Y., Kojima S., Nagahara K.,
RA Masuho Y., Ono T., Okano K., Yoshikawa Y., Aotsuka S., Sasaki N.,
RA Hattori A., Okumura K., Iwayanagi T., Ninomiya K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK074651; BAC11114.1; -.
DR HSSP; P01876; IOW0.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; C1-set; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
SQ SEQUENCE 493 AA; 53224 MW; 12ECD7B094777101 CRC64;

Query Match 76.1%; Score 67; DB 2; Length 493;
Best Local Similarity 70.6%; Pred. No. 0.016;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||:|||||
Db 69 LIWYDGTKYYSDSVKG 85

RESULT 11
QY 09UL84 PRELIMINARY; PRT; 122 AA.
ID Q9UL84;
AC Q9UL84;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Myosin-reactive immunoglobulin heavy chain variable region
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98277139; PubMed=9614934; DOI=10.1006/glin.1998.4531;
RA Wu X., Liu B., Van der Merwe P.L., Kalis N.N., Berney S.M.,
RA Young D.C.;
RT "Myosin-reactive autoantibodies in rheumatic carditis and normal
RT fetus.";
RL Clin. Immunol. Immunopathol. 87:184-192(1998).
DR EMBL; AF035030; AAD56266.1; -.
DR HSSP; P01772; 2PB4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 122
FT NON TER 122
SQ SEQUENCE 122 AA; 13579 MW; 36054D41366545B8 CRC64;

Query Match 75.0%; Score 66; DB 2; Length 122;
Best Local Similarity 81.2%; Pred. No. 0.0053;
Matches 13; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY      2 ISYDGSKKYYADSVKG 17
DB      51 ISNDGSNKFYADSVKG 66

RESULT 12
HV3L HUMAN
ID HV3L HUMAN STANDARD; PRT; 119 AA.
AC P01773;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-III region BUR.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE (MYELOMA PROTEIN BUR).
RX MEDLINE=79151016; PubMed=107164;
RA Putnam F.W., Liu Y.-S.V., Low T.L.K.;
RT "Primary structure of a human IgM immunoglobulin. IV. Streptococcal
RT IgM protease, digestion, Fab and Fc fragments, and the complete amino
RT acid sequence of the alpha 1 heavy chain."
RL J. Biol. Chem. 254:2865-2874 (1979).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02056; ALHUBR.
DR HSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Direct protein sequencing; Glycoprotein; Immunoglobulin V region;
KW Pyrrolidone carboxylic acid.
FT DOMAIN 1 112 Ig-like.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT DISULFID 22 96
FT CARBOHYD 28 28 N-linked (GlcNAc. . .).
FT NON_TER 119 119
SQ SEQUENCE 119 AA; 12981 MW; 12A709A75344D024 CRC64;

Query Match 73.9%; Score 65; DB 1; Length 119;
Best Local Similarity 70.6%; Pred. No. 0.0076;
Matches 12; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 IISYDGSKKYYADSVKG 17
DB      50 LISYGSBTFYADSVRG 66

RESULT 13
Q9ULB6
ID Q9ULB6 PRELIMINARY; PRT; 95 AA.
AC Q9ULB6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Immunoglobulin heavy chain (Fragment).
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Tange Y., Kayano H.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB035268; BAA87067.1; -.
DR PIR; PH0872; PH0872.

QY      2 ISYDGSKKYYADSVKG 17
DB      51 ISNDGSNKFYADSVKG 66

RESULT 14
HV3H HUMAN
ID HV3H HUMAN STANDARD; PRT; 122 AA.
AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig heavy chain V-III region GA.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=74175307; PubMed=4208843;
RA Florent G., Lehman D., Putnam F.W.;
RT "The switch point in mu heavy chains of human IgM immunoglobulins.";
RL Biochemistry 13:2482-2498 (1974).
CC -1- MISCELLANEOUS: This chain was isolated from a Waldenstrom's
CC macroglobulin.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A02052; M3HUGA.
DR HSP; P01772; 2FB4.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
KW Pyrrolidone carboxylic acid.
FT DOMAIN 1 112 Ig-like.
FT MOD_RES 1 1 Pyrrolidone carboxylic acid.
FT NON_TER 122 122
SQ SEQUENCE 122 AA; 13166 MW; 74E5B6959E84100A CRC64;

Query Match 72.7%; Score 64; DB 1; Length 122;
Best Local Similarity 64.7%; Pred. No. 0.011;
Matches 11; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1 IISYDGSKKYYADSVKG 17
DB      50 VISYGBBZYAAASVKG 66

RESULT 15
Q6PJA4
ID Q6PJA4 PRELIMINARY; PRT; 470 AA.
AC Q6PJA4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

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DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018747; AAH18747.1; -.
DR HSSP; P01861; IADQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; CI-set; 3.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGC1; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51715 MW; 7B49556A11FD7D99 CRC64;

Query Match 72.7%; Score 64; DB 2; Length 470;
Best Local Similarity 75.0%; Pred. No. 0.05;
Matches 12; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 ISYDGSKKYADSVKVG 17
| |||:|||||
Db 70 IKQDGSKKYVDVKVG 85

Search completed: October 14, 2005, 16:19:51
Job time : 115.156 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:00:04 ; Search time 33.4688 Seconds
(without alignments)
37.917 Million cell updates/sec

Title: US-10-614-959-11

Perfect score: 88

Sequence: 1 IISYDGSKKYYADSVKVG 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA:**
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2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88	100.0	17	4	US-09-383-667-11
2	83	94.3	17	4	US-09-383-667-18
3	82	93.2	17	4	US-09-383-667-16
4	82	93.2	17	4	US-09-383-667-20
5	82	93.2	17	4	US-09-424-840B-36
6	82	93.2	17	4	US-09-424-840B-95
7	82	93.2	17	4	US-09-424-840B-97
8	82	93.2	17	4	US-09-424-840B-108
9	82	93.2	98	1	US-08-211-202-118
10	82	93.2	115	4	US-09-726-219A-167
11	82	93.2	116	1	US-08-211-202-141
12	82	93.2	117	3	US-08-545-809A-115
13	82	93.2	119	3	US-08-331-398A-46
14	82	93.2	119	2	US-08-331-397B-46
15	82	93.2	119	2	US-08-759-804A-46
16	82	93.2	119	3	US-09-227-693-46
17	82	93.2	120	1	US-08-211-202-135
18	82	93.2	120	1	US-07-942-245-35
19	82	93.2	123	3	US-08-983-607-38
20	82	93.2	123	4	US-09-424-840B-6
21	82	93.2	128	1	US-08-478-039-96
22	82	93.2	128	1	US-08-476-349A-96
23	82	93.2	248	4	US-09-315-926A-80
24	81	92.0	17	4	US-09-424-840B-77
25	81	92.0	17	4	US-09-424-840B-111
26	81	92.0	124	4	US-09-424-840B-16
27	81	92.0	179	3	US-08-862-124-2

Sequence 102, App
Sequence 108, App
Sequence 110, App
Sequence 102, App
Sequence 108, App
Sequence 110, App
Sequence 17, Appl
Sequence 14, Appl
Sequence 12, Appl
Sequence 84, Appl
Sequence 113, App
Sequence 2, Appli
Sequence 4, Appli
Sequence 10, Appl
Sequence 22, Appl
Sequence 81, Appl
Sequence 81, Appl
Sequence 81, Appl

28 81 92.0 225 4 US-09-456-090A-102
29 81 92.0 225 4 US-09-456-090A-108
30 81 92.0 225 4 US-09-456-090A-110
31 81 92.0 225 4 US-09-453-234-102
32 81 92.0 225 4 US-09-453-234-108
33 81 92.0 225 4 US-09-453-234-110
34 81 92.0 287 3 US-08-862-124-17
35 81 92.0 304 3 US-08-862-124-14
36 79 89.8 17 4 US-09-560-198A-12
37 79 89.8 17 4 US-09-424-840B-84
38 79 89.8 17 4 US-09-424-840B-113
39 79 89.8 123 4 US-09-560-198A-2
40 79 89.8 123 4 US-09-560-198A-4
41 79 89.8 123 4 US-09-560-198A-10
42 79 89.8 123 4 US-09-424-840B-22
43 77 87.5 126 1 US-08-276-852-81
44 77 87.5 126 1 US-08-899-575-81
45 77 87.5 126 1 US-08-899-575-81

ALIGNMENTS

RESULT 1
US-09-383-667-11
; Sequence 11, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Haas, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchhofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 11
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-11

Query Match 100.0%; Score 88; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.3e-07;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKVG 17
| | | | | | | | | | | | | | | | | | | | |
Db 1 IISYDGSKKYYADSVKVG 17

RESULT 2
US-09-383-667-18
; Sequence 18, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Haas, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchhofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2

; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 18
; LENGTH: 17
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-383-667-18

Query Match 94.3%; Score 83; DB 4; Length 17;
Best Local Similarity 94.1%; Pred. No. 8,1e-07;
Matches 16; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
| | | | | | | | | | | | | | | | | | | |
Db 1 IISYDGSNKYYADSVKG 17

RESULT 3
US-09-383-667-16
; Sequence 16, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hass, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 16
; LENGTH: 17
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-383-667-16

Query Match 93.2%; Score 82; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
: | | | | | | | | | | | | | | | | | | | |
Db 1 VISYDGSNKYYADSVKG 17

RESULT 4
US-09-383-667-20
; Sequence 20, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hass, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383,667

; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 20
; LENGTH: 17
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-383-667-20

Query Match 93.2%; Score 82; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 1.2e-06;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVK 16
| | | | | | | | | | | | | | | | | | | |
Db 1 IISYDGSKKYYADSVK 16

RESULT 5
US-09-424-840B-36
; Sequence 36, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 17
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-424-840B-36

Query Match 93.2%; Score 82; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
: | | | | | | | | | | | | | | | | | | | |
Db 1 VISYDGSNKYYADSVKG 17

RESULT 6
US-09-424-840B-95
; Sequence 95, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-840B-95

Query Match 93.2%; Score 82; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 1 VISYDGSNKYYADSVKG 17

RESULT 7

US-09-424-840B-97
; Sequence 97, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 97
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-840B-97

Query Match 93.2%; Score 82; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 1 VISYDGSNKYYADSVKG 17

RESULT 8

US-09-424-840B-108
; Sequence 108, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Berchtold, Peter
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIB/IIIA RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-424-840B-108

Query Match 93.2%; Score 82; DB 4; Length 17;
Best Local Similarity 88.2%; Pred. No. 1.2e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:|||||
Db 1 VISYDGSNKYYADSVKG 17

RESULT 9

US-08-211-202-118
; Sequence 118, Application US/08211202
; Patent No. 5565332
; GENERAL INFORMATION:
; APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Matteus
; APPLICANT: BAIER, Michael
; APPLICANT: JESPEERS, Laurent Stephane Anne Therese
; APPLICANT: WINTER, Gregory Paul
; TITLE OF INVENTION: Production of chimeric antibodies - a
; TITLE OF INVENTION: combinatorial approach
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211,202
; FILING DATE: 23-SEP-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120252.3
; FILING DATE: 23-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120377.8
; FILING DATE: 25-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/31960
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 118:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 98 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-211-202-118

Query Match 93.2%; Score 82; DB 1; Length 98;
Best Local Similarity 88.2%; Pred. No. 7.3e-06;

Matches 15; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:||||| |||||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 10
US-09-726-219A-167
; Sequence 167, Application US/09726219A
; Patent No. 6806079
; GENERAL INFORMATION:
; APPLICANT: Cambridge Antibody Technology
; APPLICANT: Cambridge Antibody Technology Limited
; APPLICANT: Medical Research Council
; APPLICANT: McCafferty, John
; APPLICANT: Pope, Anthony
; APPLICANT: Johnson, Kevin
; APPLICANT: Hoogenboom, Hendricus
; APPLICANT: Griffiths, Andrew
; APPLICANT: Jackson, Ronald
; APPLICANT: Holliger, Kasper
; APPLICANT: Marks, James
; APPLICANT: Clackson, Timothy
; APPLICANT: Chiswell, David
; APPLICANT: Winter, Gregory
; APPLICANT: Bonert, Timothy
; TITLE OF INVENTION: Methods for Producing Members of Specific Binding Pairs
; FILE REFERENCE: 213839-00013
; CURRENT APPLICATION NUMBER: US/09/726,219A
; CURRENT FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: GB 9015198.6
; PRIOR FILING DATE: 1990-07-10
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9022845.3
; PRIOR FILING DATE: 1990-10-19
; PRIOR APPLICATION NUMBER: GB 9024503.6
; PRIOR FILING DATE: 1990-11-12
; PRIOR APPLICATION NUMBER: GB 9104744.9
; PRIOR FILING DATE: 1991-03-06
; PRIOR APPLICATION NUMBER: GB 9110549.4
; PRIOR FILING DATE: 1991-05-15
; PRIOR APPLICATION NUMBER: PCT/GB91/01134
; PRIOR FILING DATE: 1991-07-10
; PRIOR APPLICATION NUMBER: US 07/971,857
; PRIOR FILING DATE: 1993-01-08
; PRIOR APPLICATION NUMBER: US 08/484,893
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 272
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 167
; LENGTH: 115
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-726-219A-167

Query Match 93.2%; Score 82; DB 4; Length 115;
Best Local Similarity 88.2%; Pred. No. 8.6e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:||||| |||||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 11
US-08-211-202-141
; Sequence 141, Application US/08211202
; Patent No. 5565332
; GENERAL INFORMATION:
; APPLICANT: HOOGENBOOM, Hendricus Renerus Jacobus Mattheus
; APPLICANT: BAIER, Michael

; APPLICANT: JESPERS, Laurent Stephane Anne Therese
; APPLICANT: WINTER, Gregory Paul
; TITLE OF INVENTION: Production of chimeric antibodies - a
; NUMBER OF SEQUENCES: 144
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough, Marshall O'Toole Gerstein Murray &
; ADDRESSEE: Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211,202
; FILING DATE: 23-SEP-1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120252.3
; FILING DATE: 23-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9120377.8
; FILING DATE: 25-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/31960
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 141:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-211-202-141

Query Match 93.2%; Score 82; DB 1; Length 116;
Best Local Similarity 88.2%; Pred. No. 8.7e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 1; Gaps 0;

QY 1 IISYDGSKKYYADSVKG 17
:||||| |||||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 12
US-08-545-809A-115
; Sequence 115, Application US/08545809A
; Patent No. 6096878
; GENERAL INFORMATION:
; APPLICANT: Honjo, Tasuku
; APPLICANT: Matsuda, Fumihiko
; TITLE OF INVENTION: HUMAN IMMUNOGLOBULIN VH GENE
; TITLE OF INVENTION: SEGMENTS AND DNA FRAGMENTS CONTAINING THE SAME
; NUMBER OF SEQUENCES: 145
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA: US/08/545,809A
APPLICATION NUMBER: US/08/545,809A
FILING DATE: 27-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP93/00603
FILING DATE: 10-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Freeman, John W.
REGISTRATION NUMBER: 29,066
REFERENCE/DOCKET NUMBER: 06501/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-542-5070
TELEFAX: 617-542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 115:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-545-809A-115

Query Match 93.2%; Score 82; DB 3; Length 117;
Best Local Similarity 88.2%; Pred. No. 8.8e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYADSVK 17
Db 69 VISYDGSNKYADSVK 85

RESULT 13
US-08-331-398A-46
Sequence 46, Application US/08331398A
Patent No. 5608039
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: FitzGerald, David
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee
TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins
TITLE OF INVENTION: and Their Uses (as amended)
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,398A
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331

FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126110US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..119
OTHER INFORMATION: /note= "Human fetal immunoglobulin
OTHER INFORMATION: 56Pl'CL Variable Heavy chain (V-H)"
US-08-331-398A-46
Query Match 93.2%; Score 82; DB 1; Length 119;
Best Local Similarity 88.2%; Pred. No. 8.9e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYADSVK 17
Db 50 VISYDGSNKYADSVK 66

RESULT 14

US-08-331-397B-46
Sequence 46, Application US/08331397B
Patent No. 5981726
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Benhar, Itai
TITLE OF INVENTION: Chimeric and Mutationally Stabilized Tumor-
Specific Antibody Fragments, Fusion Proteins, and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,397B
FILING DATE: 28-OCT-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 015280-126120US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600

TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 119 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:

NAME/KEY: Protein

LOCATION: 1..119

OTHER INFORMATION: /note= "Human fetal immunoglobulin
OTHER INFORMATION: 56Pl'CL Variable Heavy chain (V-H)"
US-08-331-397B-46

Query Match 93.2%; Score 82; DB 2; Length 119;
Best Local Similarity 88.2%; Pred. No. 8.9e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:||||| |||||
Db 50 VISYDGSNKYYADSVKG 66

RESULT 15

US-08-759-804A-46
Sequence 46, Application US/08759804A
Patent No. 5990296

GENERAL INFORMATION:

APPLICANT: Pastan, Ira
APPLICANT: Willingham, Mark
APPLICANT: FitzGerald, David J.
APPLICANT: Brinkmann, Ulrich
APPLICANT: Pai, Lee

TITLE OF INVENTION: Tumor-Specific Antibody Fragments,
TITLE OF INVENTION: Fusion Proteins, and Uses Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/759,804A
FILING DATE: 03-DEC-1996
CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/331,398
FILING DATE: 28-OCT-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Ellen L.
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 015280-126140US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 46:

SEQUENCE CHARACTERISTICS:

LENGTH: 119 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:

NAME/KEY: Protein

LOCATION: 1..119

OTHER INFORMATION: /note= "Human fetal immunoglobulin
OTHER INFORMATION: 56Pl'CL Variable Heavy chain (V-H)"
US-08-759-804A-46

Query Match 93.2%; Score 82; DB 2; Length 119;
Best Local Similarity 88.2%; Pred. No. 8.9e-06;
Matches 15; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:||||| |||||
Db 50 VISYDGSNKYYADSVKG 66

Search completed: October 14, 2005, 16:22:00
Job time : 33.4688 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:20:10 ; Search time 120.859 Seconds
(without alignments)
58.615 Million cell updates/sec

Title: US-10-614-959-11

Perfect score: 88

Sequence: 1 IISYDGSKKYYADSVK 17

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1859788 seqs, 416717961 residues

Total number of hits satisfying chosen parameters: 1859788

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	87	98.9	17	18	US-10-989-462-300
2	87	98.9	121	18	US-10-989-462-262
3	87	98.9	248	10	US-09-880-748-916
4	87	98.9	248	10	US-09-880-748-916
5	87	98.9	248	10	US-09-880-748-916
6	87	98.9	248	15	US-10-293-418-1323
7	87	98.9	248	15	US-10-293-418-916
8	87	98.9	248	15	US-10-293-418-1323
9	87	98.9	251	10	US-09-880-748-1114
10	87	98.9	251	15	US-10-293-418-1114
11	87	98.9	252	18	US-10-989-462-276

12	86	97.7	135	15	US-10-364-743-97	Sequence 97, Appl
13	86	97.7	135	16	US-10-452-593-97	Sequence 97, Appl
14	84	95.5	17	9	US-09-828-708-24	Sequence 24, Appl
15	84	95.5	17	17	US-10-630-009-24	Sequence 24, Appl
16	84	95.5	101	9	US-09-828-708-10	Sequence 10, Appl
17	84	95.5	101	17	US-10-630-009-10	Sequence 10, Appl
18	84	95.5	119	14	US-10-010-729-7	Sequence 7, Appl
19	83	94.3	123	17	US-10-727-155-14	Sequence 14, Appl
20	83	94.3	125	15	US-10-292-088-58	Sequence 58, Appl
21	83	94.3	137	15	US-10-364-743-11	Sequence 11, Appl
22	83	94.3	137	15	US-10-364-743-99	Sequence 99, Appl
23	83	94.3	137	16	US-10-452-593-11	Sequence 11, Appl
24	83	94.3	137	16	US-10-452-593-99	Sequence 99, Appl
25	83	94.3	252	15	US-09-880-748-1690	Sequence 1690, Ap
26	83	94.3	252	15	US-10-293-418-1690	Sequence 1690, Ap
27	83	94.3	470	15	US-10-292-088-62	Sequence 62, Appl
28	82	93.2	17	10	US-09-972-656-48	Sequence 48, Appl
29	82	93.2	17	15	US-10-384-060-46	Sequence 46, Appl
30	82	93.2	17	15	US-10-399-701-6	Sequence 6, Appl
31	82	93.2	17	16	US-10-396-578-21	Sequence 21, Appl
32	82	93.2	17	16	US-10-396-578-39	Sequence 39, Appl
33	82	93.2	17	16	US-10-396-578-51	Sequence 51, Appl
34	82	93.2	17	16	US-10-396-578-81	Sequence 81, Appl
35	82	93.2	17	16	US-10-844-424-36	Sequence 36, Appl
36	82	93.2	17	16	US-10-844-424-95	Sequence 95, Appl
37	82	93.2	17	16	US-10-844-424-97	Sequence 97, Appl
38	82	93.2	17	16	US-10-844-424-108	Sequence 108, Appl
39	82	93.2	17	16	US-10-798-380-23	Sequence 23, Appl
40	82	93.2	17	17	US-10-726-332-114	Sequence 114, Appl
41	82	93.2	17	20	US-11-074-803-21	Sequence 21, Appl
42	82	93.2	17	20	US-11-074-803-39	Sequence 39, Appl
43	82	93.2	17	20	US-11-074-803-51	Sequence 51, Appl
44	82	93.2	17	20	US-11-074-803-81	Sequence 81, Appl
45	82	93.2	41	15	US-10-269-711-47	Sequence 47, Appl

ALIGNMENTS

RESULT 1

US-10-989-462-300

; Sequence 300, Application US/10989462

; Publication No. US20050220795A1

; GENERAL INFORMATION:

; APPLICANT: Wittrup, K. Dane

; APPLICANT: Yeung, Yik Andy

; TITLE OF INVENTION: ANTI-HYDROXYLASE ANTIBODIES AND USES

; TITLE OF INVENTION: THEREOF

; FILE REFERENCE: 01997-329001

; CURRENT APPLICATION NUMBER: US/10/989,462

; CURRENT FILING DATE: 2004-11-15

; PRIOR APPLICATION NUMBER: US 60/520,114

; PRIOR FILING DATE: 2003-11-14

; PRIOR APPLICATION NUMBER: US 60/563,514

; PRIOR FILING DATE: 2004-04-19

; NUMBER OF SEQ ID NOS: 319

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 300

; LENGTH: 17

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Synthetically generated peptide

US-10-989-462-300

Query Match 98.9%; Score 87; DB 18; Length 17;
Best Local Similarity 94.1%; Pred. No. 1.8e-06;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVK 17
:|||||

Db 1 VISYDGSKKYYADSVK 17
:|||||

RESULT 2
US-10-989-462-262
; Sequence 262, Application US/10989462
; Publication No. US20050220795A1
; GENERAL INFORMATION:
; APPLICANT: Wittrup, K. Dane
; TITLE OF INVENTION: ANTI-HYDROXYLASE ANTIBODIES AND USES
; FILE REFERENCE: 01997-329001
; CURRENT APPLICATION NUMBER: US/10/989,462
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/520,114
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US 60/563,514
; PRIOR FILING DATE: 2004-04-19
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 262
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-989-462-262

Query Match 98.9%; Score 87; DB 18; Length 121;
Best Local Similarity 94.1%; Pred. No. 1.2e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 IISYDGSKKYYADSVKG 17
Db 50 VISYDGSKKYYADSVKG 66

RESULT 3
US-09-880-748-914
; Sequence 914, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 914
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-914

Query Match 98.9%; Score 87; DB 10; Length 248;
Best Local Similarity 94.1%; Pred. No. 2.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 IISYDGSKKYYADSVKG 17
Db 50 VISYDGSKKYYADSVKG 66

RESULT 4
US-09-880-748-916
; Sequence 916, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 916
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-916

Query Match 98.9%; Score 87; DB 10; Length 248;
Best Local Similarity 94.1%; Pred. No. 2.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 IISYDGSKKYYADSVKG 17
Db 50 VISYDGSKKYYADSVKG 66

RESULT 5
US-09-880-748-1323
; Sequence 1323, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1323
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1323

Query Match 98.9%; Score 87; DB 10; Length 248;
Best Local Similarity 94.1%; Pred. No. 2.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 IISYDGSKKYYADSVKG 17
Db 50 VISYDGSKKYYADSVKG 66

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RESULT 6
US-10-293-418-914
; Sequence 914, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 914
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-914

Query Match      98.9%; Score 87; DB 15; Length 248;
Best Local Similarity 94.1%; Pred. No. 2.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 IISYDGSKKYYADSVK 17
Db      50 VISYDGSKKYYADSVK 66

RESULT 7
US-10-293-418-916
; Sequence 916, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 916
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-916

Query Match      98.9%; Score 87; DB 15; Length 248;
Best Local Similarity 94.1%; Pred. No. 2.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 IISYDGSKKYYADSVK 17
Db      50 VISYDGSKKYYADSVK 66

RESULT 8
US-10-293-418-1323
; Sequence 1323, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1323
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1323

Query Match      98.9%; Score 87; DB 15; Length 248;
Best Local Similarity 94.1%; Pred. No. 2.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 IISYDGSKKYYADSVK 17
Db      50 VISYDGSKKYYADSVK 66

RESULT 9
US-09-880-748-1114
; Sequence 1114, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
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; ORGANISM: Homo sapiens
US-10-293-418-916

Query Match      98.9%; Score 87; DB 15; Length 248;
Best Local Similarity 94.1%; Pred. No. 2.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 IISYDGSKKYYADSVK 17
Db      50 VISYDGSKKYYADSVK 66

RESULT 8
US-10-293-418-1323
; Sequence 1323, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1323
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1323

Query Match      98.9%; Score 87; DB 15; Length 248;
Best Local Similarity 94.1%; Pred. No. 2.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 IISYDGSKKYYADSVK 17
Db      50 VISYDGSKKYYADSVK 66

RESULT 9
US-09-880-748-1114
; Sequence 1114, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
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; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1114
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1114

Query Match 98.9%; Score 87; DB 10; Length 251;
Best Local Similarity 94.1%; Pred. No. 2.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSKKYYADSVKG 66

RESULT 10

US-10-293-418-1114
; Sequence 1114, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1114
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1114

Query Match 98.9%; Score 87; DB 15; Length 251;
Best Local Similarity 94.1%; Pred. No. 2.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSKKYYADSVKG 66

RESULT 11

US-10-989-462-276
; Sequence 276, Application US/10989462
; Publication No. US20050220795A1
; GENERAL INFORMATION:
; APPLICANT: Wittrup, K. Dane
; APPLICANT: Yeung, Yik Andy
; TITLE OF INVENTION: ANTI-HYDROXYLASE ANTIBODIES AND USES
; TITLE OF INVENTION: THEROF
; FILE REFERENCE: 01997-329001
; CURRENT APPLICATION NUMBER: US/10/989,462
; CURRENT FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: US 60/520,114

; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US 60/563,514
; PRIOR FILING DATE: 2004-04-19
; NUMBER OF SEQ ID NOS: 319
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 276
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-989-462-276

Query Match 98.9%; Score 87; DB 18; Length 252;
Best Local Similarity 94.1%; Pred. No. 2.5e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 50 VISYDGSKKYYADSVKG 66

RESULT 12

US-10-364-743-97
; Sequence 97, Application US/10364743
; Publication No. US20040009178A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: No. US20040009178Alan, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; FILE REFERENCE: 84 (1087-73)
; CURRENT APPLICATION NUMBER: US/10/364,743
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 97
; LENGTH: 135
; TYPE: PRT
; ORGANISM: human
US-10-364-743-97

Query Match 97.7%; Score 86; DB 15; Length 135;
Best Local Similarity 94.1%; Pred. No. 1.9e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||
Db 52 LISYDGSKKYYADSVKG 68

RESULT 13

US-10-452-593-97
; Sequence 97, Application US/10452593
; Publication No. US20040258699A1
; GENERAL INFORMATION:
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: Frederickson, Shana
; APPLICANT: Wild, Martha A.
; APPLICANT: Maruyama, Toshiaki
; APPLICANT: Nolan, Mary Jean
; TITLE OF INVENTION: IMMUNOTHERAPEUTICS FOR BIODEFENSE
; FILE REFERENCE: 98 CIP (1087-73 CIP)
; CURRENT APPLICATION NUMBER: US/10/452,593
; CURRENT FILING DATE: 2003-06-02
; PRIOR APPLICATION NUMBER: US 10/364,743
; PRIOR FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: US 60/356,086
; PRIOR FILING DATE: 2002-02-11

; PRIOR APPLICATION NUMBER: US 60/376,408
; PRIOR FILING DATE: 2002-04-29
; PRIOR APPLICATION NUMBER: US 60/428,807
; PRIOR FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 97
; LENGTH: 135
; TYPE: PRT
; ORGANISM: human
US-10-452-593-97

Query Match 97.7%; Score 86; DB 16; Length 135;
Best Local Similarity 94.1%; Pred. No. 1.9e-05;
Matches 16; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||:|||||
Db 52 LISYDGSKKYYADSVKG 68

RESULT 14

US-09-828-708-24
; Sequence 24, Application US/09828708
; Patent No. US20020146753A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US1
; CURRENT APPLICATION NUMBER: US/09/828,708
; CURRENT FILING DATE: 2001-09-24
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-828-708-24

Query Match 95.5%; Score 84; DB 9; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.7e-06;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 IISYDGSKKYYADSVKG 17
:|||||:|||||
Db 1 VISYDGNKKYYADSVKG 17

RESULT 15

US-10-630-009-24
; Sequence 24, Application US/10630009
; Publication No. US20050080239A1
; GENERAL INFORMATION:
; APPLICANT: Ditzel, H.
; APPLICANT: Burton, D.
; APPLICANT: Schaller, M.
; TITLE OF INVENTION: Autoantibodies to glucose-6-phosphate isomerase and their partici
; TITLE OF INVENTION: autoimmune disease
; FILE REFERENCE: 1361.005US2
; CURRENT APPLICATION NUMBER: US/10/630,009
; CURRENT FILING DATE: 2003-07-29
; PRIOR APPLICATION NUMBER: US 09/828,708
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-630-009-24

Query Match 95.5%; Score 84; DB 17; Length 17;
Best Local Similarity 88.2%; Pred. No. 4.7e-06;
Matches 15; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 1 IISYDGSKKYYADSVKG 17
:|||||:|||||
Db 1 VISYDGNKKYYADSVKG 17

Search completed: October 14, 2005, 17:00:42
Job time : 121.859 secs

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OM protein - protein search, using sw model

Run on: October 14, 2005, 15:51:19 ; Search time 84.5625 Seconds
(without alignments)
50.310 Million cell updates/sec

Title: US-10-614-959-12
Perfect score: 50
Sequence: 1 ASIAARVLDY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB Length	ID	Description
1	50	100.0	11	3	AA79070	AA79070 Anti-fact
2	46	92.0	11	3	AA79077	AA79077 Anti-fact
3	37	74.0	408	8	ADJ48827	ADJ48827 Oil-assoc
4	36	72.0	58	4	AAO13448	AAO13448 Human pol
5	36	72.0	652	8	ADS26132	ADS26132 Bacterial
6	36	72.0	652	8	ADS26555	ADS26555 Bacterial
7	36	72.0	655	8	ADS25373	ADS25373 Bacterial
8	36	72.0	656	8	ADS22602	ADS22602 Bacterial
9	35	70.0	708	5	ABB48560	ABB48560 Listeria
10	34	68.0	157	3	AA79070	AA79070 Zea mays
11	34	68.0	159	3	AA79070	AA79070 Zea mays
12	34	68.0	180	2	AA79070	AA79070 Amino aci
13	34	68.0	231	8	ADS28058	ADS28058 Bacterial
14	34	68.0	237	3	AA79070	AA79070 Arabidops
15	34	68.0	237	3	AA79070	AA79070 Arabidops
16	34	68.0	278	1	AA79070	AA79070 Sequence
17	34	68.0	279	1	AA79070	AA79070 Amino aci
18	34	68.0	279	2	AA79070	AA79070 Thermittas
19	34	68.0	279	2	AA79070	AA79070 Thermittas
20	34	68.0	279	2	AA79070	AA79070 Thermittas
21	34	68.0	279	2	AA79070	AA79070 Thermittas
22	34	68.0	279	2	AA79070	AA79070 Thermittas
23	34	68.0	279	2	AA79070	AA79070 Thermittas
24	34	68.0	279	2	AA79070	AA79070 Thermittas
25	34	68.0	279	2	AA79070	AA79070 Thermittas

26	34	68.0	279	2	AAW00783	Thermittas
27	34	68.0	279	2	AAW00792	Thermittas
28	34	68.0	279	2	AAW00772	Thermittas
29	34	68.0	279	2	AAW00784	Thermittas
30	34	68.0	279	2	AAW00793	Thermittas
31	34	68.0	279	2	AAW00796	Thermittas
32	34	68.0	279	2	AAW00794	Thermittas
33	34	68.0	279	2	AAW00776	Thermittas
34	34	68.0	279	2	AAW00785	Thermittas
35	34	68.0	279	2	AAW00787	Thermittas
36	34	68.0	279	2	AAW00789	Thermittas
37	34	68.0	279	2	AAW00799	Thermittas
38	34	68.0	279	2	AAW00803	Thermittas
39	34	68.0	279	2	AAW00767	Thermittas
40	34	68.0	279	2	AAW00771	Thermittas
41	34	68.0	279	2	AAW00801	Thermittas
42	34	68.0	279	2	AAW00790	Thermittas
43	34	68.0	279	2	AAW00788	Thermittas
44	34	68.0	279	2	AAW00797	Thermittas
45	34	68.0	279	2	AAW00800	Thermittas

ALIGNMENTS

RESULT 1
AA79070
ID AA79070 standard; peptide; 11 AA.
XX
AC AA79070;
XX
DT 12-JUN-2000 (first entry)
XX
DE Anti-factor IX/IXa antibody H chain V domain CDR3 amino acid sequence.
XX
KW Complementarity determining region 3; CDR3; antibody; Gla domain;
KW factor IX/IXa; blood coagulation; deep venous thrombosis;
KW arterial thrombosis; unstable angina; post myocardial infarction;
KW coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;
KW percutaneous transluminal coronary angioplasty; PTCA; inflammation;
KW septic shock; hypotension; adult respiratory distress syndrome; ARDS;
KW arterial fibrillation; disseminated intravascular coagulopathy; DIC.
XX
OS Homo sapiens.
XX
PN WO200012562-A1.
XX
PD 09-MAR-2000.

XX 26-AUG-1999; 99WO-US019453.
XX 28-AUG-1998; 98US-0098233P.
XX 03-MAR-1999; 99US-0122767P.
XX (GETH) GENENTECH INC.
XX Adams CW, Devaux B, Eaton DL, Hass PE, Judice JK, Kirchhofer D;
XX Suggett S;
XX WPI; 2000-256595/22.
XX Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-
XX carboxyglutamic acid domains useful as anti-coagulant in thrombosis,
XX stroke, and post myocardial infarction.
XX Claim 2; Fig 2; 84pp; English.

XX This sequence represents a complementarity determining region 3 (CDR3) of
XX the heavy chain variable domain of a human anti-factor IX/IXa Gla domain
XX antibody. Factor IXa is a vitamin K dependent plasma serine protease that
XX participates in the blood coagulation pathways. The Gla domain of factor
XX IXa and its zymogen factor IX contains important structural determinants
XX for interaction with high affinity binding sites on vascular endothelial

CC cells and platelets. Compositions comprising the antibodies are used for
 CC the treatment or prophylaxis of thrombotic or coagulopathic diseases or
 CC disorders in a mammal for which inhibiting a FIX/IXa mediated event is
 CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
 CC angina, post myocardial infarction, post surgical thrombosis, coronary
 CC artery bypass graft (CABG), percutaneous transluminal coronary
 CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
 CC inflammation, septic shock, hypotension, adult respiratory distress
 CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
 CC coagulopathy (DIC)
 XX
 SQ Sequence 11 AA;
 Query Match 100.0%; Score 50; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.003;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASIAAARVLDY 11
 Db 1 ASIAAARVLDY 11

RESULT 2
 AAY79077
 ID AAY79077 standard; peptide; 11 AA.
 XX
 AC AAY79077;
 XX
 DT 12-JUN-2000 (first entry)
 XX
 DE Anti-factor IX/IXa antibody H chain V domain CDR3 amino acid sequence.
 XX
 KW Complementarity determining region 3; CDR3; antibody; Gla domain;
 KW factor IX/IXa; blood coagulation; deep venous thrombosis;
 KW arterial thrombosis; unstable angina; post myocardial infarction;
 KW coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;
 KW percutaneous transluminal coronary angioplasty; PTCA; inflammation;
 KW septic shock; hypotension; adult respiratory distress syndrome; ARDS;
 KW arterial fibrillation; disseminated intravascular coagulopathy; DIC.
 XX
 OS Homo sapiens.
 XX
 FN WO200012562-A1.
 XX
 PD 09-MAR-2000.
 XX
 PF 26-AUG-1999; 99WO-US019453.
 XX
 PR 28-AUG-1998; 98US-0098233P.
 PR 03-MAR-1999; 99US-0122767P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Adams CW, Devaux B, Eaton DL, Hass PE, Judice JK, Kirchhofer D;
 PI Suggett S;
 XX
 DR WPI; 2000-256595/22.
 XX
 PT Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-
 PT carboxylglutamic acid domains useful as anti-coagulant in thrombosis,
 PT stroke, and post myocardial infarction.
 XX
 PS Claim 2; Fig 2; 84pp; English.
 XX
 CC This sequence represents a complementarity determining region 3 (CDR3) of
 CC the heavy chain variable domain of a human anti-factor IX/IXa Gla domain
 CC antibody. Factor IXa is a vitamin K dependent plasma serine protease that
 CC participates in the blood coagulation pathways. The Gla domain of factor
 CC IXa and its zymogen factor IX contains important structural determinants
 CC for interaction with high affinity binding sites on vascular endothelial
 CC cells and platelets. Compositions comprising the antibodies are used for
 CC the treatment or prophylaxis of thrombotic or coagulopathic diseases or
 CC disorders in a mammal for which inhibiting a FIX/IXa mediated event is

CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
 CC angina, post myocardial infarction, post surgical thrombosis, coronary
 CC artery bypass graft (CABG), percutaneous transluminal coronary
 CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
 CC inflammation, septic shock, hypotension, adult respiratory distress
 CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
 CC coagulopathy (DIC)
 XX
 SQ Sequence 11 AA;
 Query Match 92.0%; Score 46; DB 3; Length 11;
 Best Local Similarity 90.9%; Pred. No. 0.019;
 Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASIAAARVLDY 11
 Db 1 ASIAAARVLDY 11

RESULT 3
 ADJ48827
 ID ADJ48827 standard; protein; 408 AA.
 XX
 AC ADJ48827;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Oil-associated gene related protein #327.
 XX
 KW oil-associated gene; transgenic; enhanced seed oil; vegetable oil.
 XX
 OS Unidentified.
 XX
 FN US2004025202-A1.
 XX
 PD 05-FEB-2004.
 XX
 PF 14-MAR-2003; 2003US-00389566.
 PR 15-MAR-2002; 2002US-0365301P.
 PR 26-JUN-2002; 2002US-0391786P.
 PR 26-JUN-2002; 2002US-0392018P.
 XX
 PA (LAUR/) LAURIE C C.
 PA (RAVA/) RAVANELLO M.
 PA (SAVA/) SAVAGE T.
 PA (LEDE/) LEDEAUX J R.
 PA (ROGE/) ROGERS J A.
 XX
 PI Laurie CC, Ravanello M, Savage T, Ledeaux JR, Rogers JA;
 XX
 DR WPI; 2004-142683/14.
 XX
 PT Novel recombinant DNA construct comprising a promoter functional in
 PT plants operably linked to an oil-associated gene for producing transgenic
 PT plant seed.
 XX
 PS Example 3; SEQ ID NO 831; 22pp; English.
 XX
 CC The invention relates to a recombinant DNA construct comprising a
 CC promoter functional in plants operably linked to an oil-associated gene.
 CC The construct is useful for transgenic plant seed which has in its genome
 CC the construct, that is functional in the plant to transcribe the oil-
 CC associated gene. The transgenic plant seed grows into a plant having
 CC enhanced seed oil as compared to wild type. The construct is useful for
 CC producing hybrid maize seed. The transgenic plant seed is useful for
 CC producing vegetable oil. The present sequence represents the amino acid
 CC sequence of an oil-associated gene related protein.
 XX
 SQ Sequence 408 AA;
 Query Match 74.0%; Score 37; DB 8; Length 408;
 Best Local Similarity 80.0%; Pred. No. 62;


```
Db          255 AATAAARAIDY 265
           |: ||||| :||
RESULT 6
ID ADS25655 standard; protein; 652 AA.
XX
XX
AC ADS25655;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #14688.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 14688; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
```

```
SQ Sequence 652 AA;
Query Match 72.0%; Score 36; DB 8; Length 652;
Best Local Similarity 63.6%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ASIAAARVLDY 11
   |: ||||| :||
Db 255 AATAAARAIDY 265
RESULT 7
ID ADS25373 standard; protein; 655 AA.
XX
XX ADS25373;
AC ADS25373;
XX
DT 02-DEC-2004 (first entry)
XX
DE Bacterial polypeptide #14406.
XX
KW Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant disease resistance;
KW cell cycle pathway modification; plant growth regulator;
KW homologous recombination; seed oil yield; protein yield; carbohydrate;
KW nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX
OS Bacteria.
XX
PN US2003233675-A1.
XX
PD 18-DEC-2003.
XX
PF 20-FEB-2003; 2003US-00369493.
XX
PR 21-FEB-2002; 2002US-0360039P.
XX
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX
PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
PT New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX
PS Claim 1; SEQ ID NO 14406; 122pp; English.
XX
CC The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
```

CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 655 AA;

Query Match 72.0%; Score 36; DB 8; Length 655;
 Best Local Similarity 63.6%; Pred. No. 1.6e+02;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTAARVLDY 11

| : |||| : ||

Db 255 AATAARAIDY 265

RESULT 8

ADS22602

ID ADS22602 standard; protein; 656 AA.

XX AC ADS22602;

XX DT 02-DEC-2004 (first entry)

XX DE Bacterial polypeptide #11635.

XX KW Recombinant DNA construct; transformed plant; improved plant property;
 XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
 XX pathogen tolerance; pest tolerance; plant disease resistance;
 XX cell cycle pathway modification; plant growth regulator;
 XX homologous recombination; seed oil yield; protein yield; carbohydrate;
 XX nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
 XX bacterial polypeptide.

XX OS Bacteria.

XX US2003233675-A1.

XX PN 18-DEC-2003.

XX PF 20-FEB-2003; 2003US-00369493.

XX PR 21-FEB-2002; 2002US-0360039P.

XX PA (CAO Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
 XX (HINKLE G J,
 XX (SLATER S C,
 XX (CHEN X,
 XX (GOLDMAN B S.

XX PI Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;

XX WPI; 2004-061375/06.

XX DR New recombinant DNA construct comprising a promoter positioned to provide
 XX for expression of a polynucleotide encoding a polypeptide from a
 XX microbial source, useful for producing plants with improved properties.

XX PS Claim 1; SEQ ID NO 11635; 122pp; English.

XX CC The invention relates to a recombinant DNA construct comprising a
 XX promoter functional in a plant cell, where the promoter is positioned to
 XX provide for expression of a polynucleotide encoding a polypeptide from a
 XX microbial source. The invention also relates to a transformed plant
 XX comprising the recombinant DNA construct and a method of producing a
 XX transformed plant having an improved property. The plant is a crop plant
 XX such as maize or soybean. The method of producing a transformed plant
 XX having an improved property comprises transforming a plant with the
 XX recombinant DNA construct and growing the transformed plant, where the
 XX polynucleotide or polypeptide is useful for improving plant properties.
 XX The recombinant DNA construct is useful for producing plants with

CC improved plant properties, e.g. improved cold, heat or drought tolerance,
 CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
 CC increased resistance to plant disease, better growth rate by modification
 CC of the cell cycle pathway with plant growth regulators, increased rate of
 CC homologous recombination, modified seed oil or protein yield and/or
 CC content, improved yield by modification of carbohydrate, nitrogen or
 CC phosphorus use and/or uptake, by modification of photosynthesis or by
 CC providing improved plant growth and development under at least one stress
 CC condition, improved lignin production or improved galactomannan
 CC production. This sequence represents a bacterial polypeptide used in the
 CC scope of the invention. Note: The sequence data for this patent did not
 CC form part of the printed specification but was obtained in electronic
 CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 656 AA;

Query Match 72.0%; Score 36; DB 8; Length 656;
 Best Local Similarity 63.6%; Pred. No. 1.7e+02;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAARVLDY 11

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Db 255 AATAARAIDY 265

RESULT 9

ABB48560

ID ABB48560 standard; protein; 708 AA.

XX AC ABB48560;

XX DT 05-FEB-2002 (first entry)

XX DE Listeria monocytogenes protein #1264.

XX KW Antibacterial; gene therapy; vaccine; biosynthesis; biodegradation;
 XX vitamin B12; bacterial infection; disease.

XX OS Listeria monocytogenes.

XX PN WO200177335-A2.

XX PD 18-OCT-2001.

XX PF 11-APR-2001; 2001WO-FR001118.

XX PR 11-APR-2000; 2000FR-00004629.

XX PA (INSP) INST PASTEUR.

XX PI Buchrieser C, Frangeul L, Couve E, Rusniok C, Fsihi H, Dehoux P;
 XX Dussurget O, Chetouani F, Nedjari H, Glaser P, Kunst F, Cossart P;
 XX Daniels J, Goebel W, Kreft J, Kuhn M, Ng E, Vazquez-Boland JA;
 XX Dominguez-Bernal G, Garrido-Garcia P, Tierrez-Martinez A, Amend A;
 XX Chakraborty T, Dommann E, Hain T, Berche P, Charbit A, Durant L;
 XX Perez-Diaz J, Baquero F, Garcia Del Portillo F, Gomez-Lopez N;
 XX Maduenio E, De Pablos B, Wehland J, Kaerst U, Entian K, Hauf J;
 XX Rose M, Voss H;
 XX WPI; 2002-010914/01.

XX PT Genomic sequence for Listeria monocytogenes, useful e.g. for treatment
 XX and prevention of Listeria and related bacterial infections, and related
 XX polypeptides.

XX PS Claim 6; SEQ ID NO 1265; 192pp; French.

XX CC The present invention relates to the genome sequence of Listeria
 XX monocytogenes EGD-e (see ABA03041). The genome sequence and fragments of
 XX it are useful for selecting probes and primers for detecting genes in L.
 XX monocytogenes and related organisms, and for studying genetic
 XX polymorphisms and other genomes. The present sequence is a protein
 XX encoded by the genome sequence of the present invention. Proteins

CC expressed from the genome sequence are useful for raising specific
CC antibodies. Identification of L. monocytogenes and related organisms, and
CC for biosynthesis and biodegradation, especially biosynthesis of Vitamin
CC B12. The genome sequence and proteins encoded by it are also useful for
CC selecting compounds that regulate gene expression and cell replication
CC and modulate L. monocytogenes-related diseases. In addition, the genome
CC sequence and proteins encoded by it are useful in pharmaceutical and
CC vaccines compositions for the treatment or prevention of infections by L.
CC monocytogenes and related organisms. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 708 AA;

Query Match 70.0%; Score 35; DB 5; Length 708;
Best Local Similarity 75.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 AAARVLDY 11

Db 697 AAARIIDY 704

RESULT 10

AAAG18510
ID AAG18510 standard; protein; 157 AA.

XX AC AAG18510;

XX DT 17-OCT-2000 (first entry)

XX DE Zea mays protein fragment SEQ ID NO: 19948.

KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.

XX OS Zea mays subsp. mays.

XX PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-00301439.

XX PR 25-FEB-1999; 99US-0121825P.

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Query Match 68.0%; Score 34; DB 3; Length 157;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AARVLDY 11
Db 117 AARVLDY 123
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AAG18509
ID AAG18509 standard; protein; 159 AA.
XX
AC AAG18509;
XX
DT 17-OCT-2000 (first entry)
XX
DE Zea mays protein fragment SEQ ID NO: 19947.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-00301439.
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Query Match      68.0%; Score 34; DB 3; Length 159;
Best Local Similarity 100.0%; Pred. No. 91;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 AARVLDY 11
Db 119 AARVLDY 125
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RESULT 12
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AC AAY37904;
XX
XX 07-OCT-1999 (first entry)
XX
XX Amino acid sequence of a Chlamydia trachomatis protein.
DE
XX Vaccine; eye disease; conventional trachoma; nonendemic trachoma;
KW paratrachoma; inclusion conjunctivitis; genital disease; perihhepatitis;
KW nongonococcal urethritis; epididymitis; cervicitis; salpingitis;
KW bartholinitis; pneumopathy; venereal lymphogranulomatosis.
XX Chlamydia trachomatis.
OS
XX WO9928475-A2.
XX
XX 10-JUN-1999.
XX
XX 27-NOV-1998; 98WO-IB001939.
XX
XX 28-NOV-1997; 97FR-00015041.
XX
XX 17-DEC-1997; 97FR-00016034.
XX
XX 04-NOV-1998; 98US-0107077P.
XX
XX (GEST ) GENSET.
XX
XX Griffais R;
XX
XX WPI; 1999-371125/31.
XX
XX Genome sequence of Chlamydia trachomatis.
XX
XX Disclosure; Page 1426; 1755pp; English.
XX
XX AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome
CC of Chlamydia trachomatis (see AA01425). The polypeptides can be used as
CC vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences
CC can also be used to control growth of the microorganism. Chlamydia
CC trachomatis is responsible for a large number of diseases, e.g. eye
CC diseases such as conventional trachoma, nonendemic trachoma,
CC paratrachoma, and inclusion conjunctivitis; genital diseases such as
CC nongonococcal urethritis, epididymitis, cervicitis, salpingitis,
CC perihhepatitis, bartholinitis; pneumopathy in breast feeding infants; and
CC venereal lymphogranulomatosis. The polypeptides of the invention may be
CC of use in treating these diseases
XX
XX Sequence 180 AA;
XX
XX Query Match      68.0%; Score 34; DB 2; Length 180;
XX Best Local Similarity 77.8%; Pred. No. 1e+02;
XX Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 IAAARVLDY 11
Db 140 IAAARVLDY 148
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RESULT 13
ADS28058
ID ADS28058 standard; protein; 231 AA.

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XX ADS28058;
AC 02-DEC-2004 (first entry)
XX Bacterial polypeptide #17091.
XX
XX Recombinant DNA construct; transformed plant; improved plant property;
XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
XX pathogen tolerance; pest tolerance; plant disease resistance;
XX cell cycle pathway modification; plant growth regulator;
XX homologous recombination; seed oil yield; protein yield; carbohydrate;
XX nitrogen; phosphorus; photosynthesis; lignin; galactomannan;
XX bacterial polypeptide.
XX Bacteria.
XX
XX US2003233675-A1.
XX
XX 18-DEC-2003.
XX
XX 20-FEB-2003; 2003US-00369493.
XX
XX 21-FEB-2002; 2002US-0360039P.
XX
XX (CAOY/) CAO Y.
XX (HINK/) HINKLE G J.
XX (SLAT/) SLATER S C.
XX (CHEN/) CHEN X.
XX (GOLD/) GOLDMAN B S.
XX
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
XX WPI; 2004-061375/06.
XX
XX New recombinant DNA construct comprising a promoter positioned to provide
XX for expression of a polynucleotide encoding a polypeptide from a
XX microbial source, useful for producing plants with improved properties.
XX
XX Claim 1; SEQ ID NO 17091; 122pp; English.
XX
XX The invention relates to a recombinant DNA construct comprising a
XX promoter functional in a plant cell, where the promoter is positioned to
XX provide for expression of a polynucleotide encoding a polypeptide from a
XX microbial source. The invention also relates to a transformed plant
XX comprising the recombinant DNA construct and a method of producing a
XX transformed plant having an improved property. The plant is a crop plant
XX such as maize or soybean. The method of producing a transformed plant
XX having an improved property comprises transforming a plant with the
XX recombinant DNA construct and growing the transformed plant, where the
XX polynucleotide or polypeptide is useful for improving plant properties.
XX The recombinant DNA construct is useful for producing plants with
XX improved plant properties, e.g. improved cold, heat or drought tolerance,
XX tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
XX increased resistance to plant disease, better growth rate by modification
XX of the cell cycle pathway with plant growth regulators, increased rate of
XX homologous recombination, modified seed oil or protein yield and/or
XX content, improved yield by modification of carbohydrate, nitrogen or
XX phosphorus use and/or uptake, by modification of photosynthesis or by
XX providing improved plant growth and development under at least one stress
XX condition, improved lignin production or improved galactomannan
XX production. This sequence represents a bacterial polypeptide used in the
XX scope of the invention. Note: The sequence data for this patent did not
XX form part of the printed specification but was obtained in electronic
XX format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX Sequence 231 AA;
XX
XX Query Match      68.0%; Score 34; DB 8; Length 231;
XX Best Local Similarity 80.0%; Pred. No. 1.4e+02;
XX Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAARVLD 10

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XX      DT      17-OCT-2000 (first entry)
XX      DE      Arabidopsis thaliana protein fragment SEQ ID NO: 22440.
XX      KW      Protein identification; signal transduction pathway; metabolic pathway;
KW      hybridisation assay; genetic mapping; gene expression control; promoter;
KW      termination sequence.
XX      OS      Arabidopsis thaliana.
XX      PN      EP1033405-A2.
XX      PD      06-SEP-2000.
XX      PF      25-FEB-2000; 2000EP-00301439.
XX      PR      25-FEB-1999; 99US-0121825P.
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Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AARVLDY 11
Db 8 AARVLDY 14
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RESULT 15
AAG51887
ID AAG51887 standard; protein; 237 AA.
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XX AAG51887;
AC
XX
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65899.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
XX Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-00301439.
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PR 21-OCT-1999; 99US-0160741P.
PR 21-OCT-1999; 99US-0160767P.
PR 21-OCT-1999; 99US-0160768P.
PR 21-OCT-1999; 99US-0160770P.
PR 21-OCT-1999; 99US-0160814P.
PR 21-OCT-1999; 99US-0160815P.
PR 22-OCT-1999; 99US-0160980P.
PR 22-OCT-1999; 99US-0160981P.
PR 22-OCT-1999; 99US-0160989P.
PR 25-OCT-1999; 99US-0161404P.
PR 25-OCT-1999; 99US-0161405P.
PR 25-OCT-1999; 99US-0161406P.
PR 26-OCT-1999; 99US-0161359P.
PR 26-OCT-1999; 99US-0161360P.
PR 26-OCT-1999; 99US-0161361P.
PR 28-OCT-1999; 99US-0161920P.
PR 28-OCT-1999; 99US-0161992P.
PR 28-OCT-1999; 99US-0161993P.
PR 29-OCT-1999; 99US-0162142P.

Query Match 68.0%; Score 34; DB 3; Length 237;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AARVLDY 11
| | | | |
Db 8 AARVLDY 14

Search completed: October 14, 2005, 16:12:40
Job time : 85.5625 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:02:59 ; Search time 15.2969 Seconds
(without alignments)
69.190 Million cell updates/sec

Title: US-10-614-959-12
Perfect score: 50
Sequence: 1 ASTAAARVLDY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79.*

1: pir1.*

2: pir2.*

3: pir3.*

4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	36	72.0	663	2 AF2984	3-methylcrotonyl-C
2	36	72.0	709	2 A98299	3-methylcrotonyl-C
3	35	70.0	143	2 S43071	hypothetical prote
4	35	70.0	692	2 S56849	probable membrane
5	35	70.0	696	2 A51210	teichoic acid bios
6	34	68.0	231	2 D87715	carboxymethyleneb
7	34	68.0	279	1 SUMYTV	thermitase (EC 3.4
8	34	68.0	579	2 I40371	methyltransferase
9	34	68.0	649	2 T38883	hypothetical prote
10	34	68.0	956	2 B71468	probable insulinas
11	33	66.0	162	2 AF1059	probable transcrip
12	33	66.0	202	2 AF2831	DNA polymerase III
13	33	66.0	202	2 B97609	probable DNA polym
14	33	66.0	220	2 F9878	conserved hypochet
15	33	66.0	264	2 G59213	hypothetical prote
16	33	66.0	358	2 T45400	hypothetical prote
17	33	66.0	367	2 C70858	hypothetical prote
18	33	66.0	397	2 C84904	hypothetical prote
19	33	66.0	441	2 A75619	cobyrinic acid a,c
20	33	66.0	482	2 H70463	glycine dehydrogen
21	33	66.0	509	2 G82104	glutamyl-tRNA synt
22	33	66.0	614	2 S45053	membrane protein E
23	33	66.0	1027	2 T27970	hypothetical prote
24	33	66.0	1232	2 T06165	multidrug resistan
25	32	64.0	305	2 E85437	methionyl aminopep
26	32	64.0	342	2 G69502	histidinyl-phospha
27	32	64.0	363	2 D64640	hypothetical prote
28	32	64.0	365	2 C87712	carbohydrate kinas
29	32	64.0	409	2 AG2869	N-carbamoyl-beta-a

30	32	64.0	415	2 A97646	n-carbamoyl-beta-a
31	32	64.0	435	2 T20819	hypothetical prote
32	32	64.0	448	2 T16256	hypothetical prote
33	32	64.0	576	1 B70558	probable ABC trans
34	32	64.0	655	2 G96524	protein TINI5.9 [i
35	32	64.0	777	2 G95940	probable xanthine
36	32	64.0	817	2 T49642	hypothetical prote
37	31	62.0	119	2 T16347	hypothetical prote
38	31	62.0	131	2 AG2388	hypothetical prote
39	31	62.0	144	2 C75376	hypothetical prote
40	31	62.0	172	2 S75615	hypothetical prote
41	31	62.0	177	2 B83036	probable bacteriof
42	31	62.0	230	2 AF3541	glutathione transf
43	31	62.0	249	2 A81001	electron transfer
44	31	62.0	249	2 F82018	electron transfer
45	31	62.0	254	2 AC3018	conserved hypothet

ALIGNMENTS

RESULT 1

AF2984

3-methylcrotonyl-CoA carboxylase alpha subunit [imported] - Agrobacterium tumefaciens (s

C;Species: Agrobacterium tumefaciens

C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004

C;Accession: AF2984

R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L.
erage, G.; Gillet, W.; Grant, C.; Guenthrner, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.

Science 294, 2317-2323, 2001

A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.

A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.

A;Reference number: AB2577; MUID:21608550; PMID:11743193

A;Accession: AF2984

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-663 <KUR>

A;Cross-references: UNIPROT:Q8UA95; GB:AB008689; PIDN:AAL44292.1; PID:gi7741880; GSPDB:G

A;Experimental source: strain C58 (Dupont)

C;Genetics:

A;Gene: mcca

A;Map position: linear chromosome

C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoy

Query Match 72.0%; Score 36; DB 2; Length 663;

Best Local Similarity 63.6%; Pred.No. 27;

Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTAAARVLDY 11

| : | | | | : | |

Db 258 AATTAARAIDY 268

RESULT 2

A98299

3-methylcrotonyl-CoA carboxylase alpha chain (AF310338) [imported] - Agrobacterium tumef

C;Species: Agrobacterium tumefaciens

C;Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 09-Jul-2004

C;Accession: A98299

R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;

Science 294, 2323-2328, 2001

A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum

A;Reference number: A97359; MUID:21608551; PMID:11743194

A;Accession: A98299

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-709 <KUR>

A;Cross-references: UNIPROT:Q8UA95; GB:AB007870; PIDN:AAK89915.1; PID:gi15159866; GSPDB:G

C;Genetics:

A;Gene: AGR_L_2704

A;Map position: linear chromosome
C;Superfamily: propionyl-CoA carboxylase alpha chain; biotin carboxylase homology; lipoyl

Query Match 72.0%; Score 36; DB 2; Length 709;
Best Local Similarity 63.6%; Pred. No. 29;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAAARVLDY 11
I:|||||:
Db 304 AATAARAIDY 314

RESULT 3
S43071
hypothetical protein 5 - human herpesvirus 6
C;Species: human herpesvirus 6
C;Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C;Accession: S43071
R;Thompson, J.; Choudhury, S.; Kashanchi, F.; Doniger, J.; Berneman, Z.; Frenkel, N.; Ro
Oncogene 9, 1167-1175, 1994
A;Title: A transforming fragment within the direct repeat region of human herpesvirus ty
A;Reference number: S43067; MUID:94181269; PMID:8134119
A;Accession: S43071
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-143 <THO>
A;Cross-references: UNIPROT:O69582; EMBL:X73675; NID:9469952; PIDN:CAA52028.1; PID:94699
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1993

Query Match 70.0%; Score 35; DB 2; Length 143;
Best Local Similarity 88.9%; Pred. No. 8.7;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASIAAARVL 9
I:|||||:
Db 7 ASIAAARVL 15

RESULT 4
S56849
probable membrane protein YJL073w - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein HRC558; hypothetical protein J1083
C;Species: Saccharomyces cerevisiae
C;Date: 05-May-1995 #sequence_revision 08-Sep-1995 #text_change 09-Jul-2004
C;Accession: S56849; S56847; S50798; S47117; S57736
R;Rose, M.; Koetex, P.; Entian, K.D.
submitted to the Protein Sequence Database, September 1995
A;Reference number: S56848
A;Accession: S56849
A;Molecule type: DNA
A;Residues: 1-692 <ROS>
A;Cross-references: UNIPROT:P40358; EMBL:Z49348; NID:g1008228; PID:g1008229; MIPS:YJL073
R;Vandenbol, M.; Durand, P.; Portetelle, D.; Hilger, F.
submitted to the Protein Sequence Database, September 1995
A;Reference number: S56835
A;Accession: S56847
A;Molecule type: DNA
A;Residues: 135-692 <POH>
A;Cross-references: EMBL:Z49348; MIPS:YJL073w
R;Vandenbol, M.; Durand, P.; Dion, C.; Portetelle, D.; Hilger, F.
Yeast 11, 57-60, 1995
A;Title: Sequence of a 17.1 kb DNA fragment from chromosome X of Saccharomyces cerevisiae
A;Reference number: S50798; MUID:95282514; PMID:7762302
A;Accession: S50798
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 135-692 <VAN>
A;Cross-references: EMBL:Z34288; NID:g498992; PIDN:CAA84049.1; PID:g498993
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1994
R;Vandenbol, M.; Durand, P.; Dion, C.; Portetelle, D.; Hilger, F.
submitted to the EMBL Data Library, June 1994
A;Description: Sequence analysis of a 17.1 kb DNA fragment from chromosome X of Sacchard
A;Reference number: S47117

A;Accession: S47117
A;Molecule type: DNA
A;Residues: 135-692 <VAV>
A;Cross-references: EMBL:Z34288; NID:g498992; PID:g498993
R;Sor, F.J.
submitted to the EMBL Data Library, June 1995
A;Reference number: S57731
A;Accession: S57736
A;Molecule type: DNA
A;Residues: 1-692 <SOR>
A;Cross-references: EMBL:X88851; NID:g895892; PID:g895898
C;Genetics:
A;Gene: SGD:JEM1
A;Cross-references: SGD:S0003609; MIPS:YJL073w
A;Map position: 10L
C;Keywords: transmembrane protein
F;585-695/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 70.0%; Score 35; DB 2; Length 692;
Best Local Similarity 70.0%; Pred. No. 45;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SIAAARVLDY 11
I:|||||:
Db 245 SLAAAIIIDY 254

RESULT 5
AB1210
teichoic acid biosynthesis protein B homolog lmo1085 [imported] - Listeria monocytogenes
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C;Accession: AB1210
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A;Title: Comparative genomics of Listeria species.
A;Reference number: AB1077; MUID:21537279; PMID:11679669
A;Accession: AB1210
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-696 <GLA>
A;Cross-references: UNIPROT:Q8Y833; GB:NC_003210; PIDN:CAC99163.1; PID:g16410487; GSPDB
A;Experimental source: strain EGD-e
C;Genetics:
A;Gene: lmo1085

Query Match 70.0%; Score 35; DB 2; Length 696;
Best Local Similarity 75.0%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 AAARVLDY 11
I:|||||:
Db 685 AAARIIDY 692

RESULT 6
D87715
carboxymethylenebutenolidase [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: D87715
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: AB7249; MUID:21173698; PMID:11259647
A;Accession: D87715
A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-231 <STO>
A;Cross-references: UNIPROT:Q9A213; GB:AB005673; NID:g13425534; PIDN:AAK25720.1; GSPDB:Q9A213
C;Species: carboxymethylglutaminase
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38883
C;Superfamily: carboxymethylglutaminase

Query Match 68.0%; Score 34; DB 2; Length 231;
Best Local Similarity 80.0%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASTAAARVLD 10
|:|||||
Db 100 ATIAAARKLD 109

RESULT 7
SUMYTV
Thermotase (EC 3.4.21.66) - Thermoactinomyces vulgaris
C;Species: Thermoactinomyces vulgaris
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004
C;Accession: A00973
R;Meloun, B.; Baudys, M.; Kostka, V.; Hausdorf, G.; Frommel, C.; Hohn, W.E.
FEBS Lett. 183, 195-200, 1985
A;Title: Complete primary structure of thermitase from Thermoactinomyces vulgaris and its
A;Reference number: A00973
A;Accession: A00973
A;Molecule type: protein
A;Residues: 1-279 <MEL>
A;Cross-references: UNIPROT:P04072
C;Comment: This protein is enzymatically similar to a proteinase from Streptomyces sp.
C;Superfamily: subtilisin; subtilisin homology
C;Keywords: hydrolase; serine proteinase
F;29-239/Domain: subtilisin homology <SBT>
F;38,71,225/Active site: Asp, His, Ser #status predicted

Query Match 68.0%; Score 34; DB 1; Length 279;
Best Local Similarity 80.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASTAAARVLD 10
|:|||||
Db 96 ASILAVRVD 105

RESULT 8
I40371
methyltransferase - Bacillus stearothermophilus (fragment)
C;Species: Bacillus stearothermophilus
C;Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 09-Jul-2004
C;Accession: I40371
R;Rina, M.; Markaki, M.; Bouriotis, V.
Gene 150, 71-73, 1994
A;Title: Sequence of the cloned bscIM gene: M.BscI reveals high homology to M.BanIII.
A;Reference number: I40371; MUID:95047552; PMID:7959066
A;Accession: I40371
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-579 <RES>
A;Cross-references: UNIPROT:P43423; EMBL:X79509; NID:g619638; PIDN:CAA56041.1; PID:g619638
C;Species: bscIM
C;Superfamily: site-specific methyltransferase (adenine-specific) Paer71

Query Match 68.0%; Score 34; DB 2; Length 579;
Best Local Similarity 54.5%; Pred. No. 60;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ASTAAARVLD 11
|:|||||
Db 26 AEVIARVLD 36

RESULT 9
T38883
hypothetical protein SPAC4H3.03c - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: T38883
R;Murphy, L.; Harris, D.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, February 1996
A;Reference number: Z21807
A;Accession: T38883
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-649 <MUR>
A;Cross-references: UNIPROT:Q10211; EMBL:Z69380; PIDN:CAA93342.1; GSPDB:GN00066; SPDB:SPAC4H3.03c
A;Experimental source: strain 972h-; cosmid c4H3
C;Genetics:
A;Gene: SPDB:SPAC4H3.03c
A;Map position: 1
C;Superfamily: Schizosaccharomyces pombe hypothetical protein SPAC4H3.03c

Query Match 68.0%; Score 34; DB 2; Length 649;
Best Local Similarity 70.0%; Pred. No. 68;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASTAAARVLD 10
|:|||||
Db 631 AAIAAAHILD 640

RESULT 10
B71468
probable insulinase family/proteinase III - Chlamydia trachomatis (serotype D, strain UW 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C;Species: Chlamydia trachomatis
C;Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C;Accession: B71468
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell, S.
Science 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis
A;Reference number: A71570; MUID:9900809; PMID:9784136
A;Accession: B71468
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-956 <ARN>
A;Cross-references: UNIPROT:O84812; GB:AB001353; NID:g3329271; PIDN:AAAC6840
A;Experimental source: serotype D, strain UW-3/Cx
C;Genetics:
A;Gene: ptr
C;Superfamily: insulin-degrading enzyme (IDE)

Query Match 68.0%; Score 34; DB 2; Length 956;
Best Local Similarity 77.8%; Pred. No. 1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 IAAARVLDY 11
|:|||||
Db 916 IAAARSMYD 924

RESULT 11
AF1059
probable transcription regulator STY4801 [imported] - Salmonella enterica subsp. enterica
C;Species: Salmonella enterica subsp. enterica serovar Typhi
C;Note: This species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AF1059
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AF1059

A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-162 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD06923.1; PID:gl6505571; GSPDB:GN00176
C:Genetics:
A:Gene: STY4801

Query Match 66.0%; Score 33; DB 2; Length 162;
Best Local Similarity 75.0%; Pred. No. 26;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 AAARVLDY 11
| | | | |
Db 112 AVARILDY 119

RESULT 12
AF2831
DNA polymerase III, epsilon subunit [imported] - Agrobacterium tumefaciens (strain C58,
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C:Accession: AF2831
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AF2831
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-202 <KUR>
A:Cross-references: UNIPROT:Q8UDP4; GB:AE008688; PIDN:AAL43068.1; PID:gl7740536; GSPDB:G
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: Atu2077
A:Map position: circular chromosome

Query Match 66.0%; Score 33; DB 2; Length 202;
Best Local Similarity 88.9%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAARVL 9
| | | | |
Db 156 ASIAAARAL 164

RESULT 13
B97609
probable DNA polymerase III, epsilon chain [imported] - Agrobacterium tumefaciens (strain
C:Species: Agrobacterium tumefaciens
C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
C:Accession: B97609
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Quorollo, B.; Goldman,
A.; Liu, F.; Wolam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: B97609
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-202 <KUR>
A:Cross-references: UNIPROT:Q8UDP4; GB:AE007869; PIDN:AAK87827.1; PID:gl5157207; GSPDB:G
C:Genetics:
A:Gene: AGR_C 3764
A:Map position: circular chromosome

Query Match 66.0%; Score 33; DB 2; Length 202;
Best Local Similarity 88.9%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAARVL 9
| | | | |
Db 156 ASIAAARAL 164

RESULT 14
F89878
conserved hypothetical protein SA0939 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: F89878
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: F89878
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-220 <KUR>
A:Cross-references: UNIPROT:Q99V10; GB:BA000018; PID:gl3700889; PIDN:BAR42185.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA0939
C:Superfamily: conserved hypothetical protein MG323

Query Match 66.0%; Score 33; DB 2; Length 220;
Best Local Similarity 60.0%; Pred. No. 35;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 SIARVLDY 11
: : : : :
Db 131 NVASVLDY 140

RESULT 15
G69213
hypothetical protein MTH852 - Methanobacterium thermoautotrophicum (strain Delta H)
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Jul-2004
C:Accession: G69213
R:Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
; Qiu, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiواني, N.
ki, S.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
J. Bacteriol. 179, 7135-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: funct
A:Reference number: A69000; MUID:98037514; PMID:9371463
A:Accession: G69213
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-264 <MTH>
A:Cross-references: UNIPROT:O26940; GB:AE000862; GB:AE000666; NID:g2621943; PIDN:AAB8535
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MTH852

Query Match 66.0%; Score 33; DB 2; Length 264;
Best Local Similarity 54.5%; Pred. No. 43;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAARVLDY 11
| | | | : : : :
Db 94 ASIAAVKLINY 104

Search completed: October 14, 2005, 16:23:38
Job time : 17.2969 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 15:51:44 ; Search time 73.2188 Seconds
(without alignments)
76.932 Million cell updates/sec

Title: US-10-614-959-12
Perfect score: 50
Sequence: 1 ASIATAARVLDY 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	37	74.0	421	2 Q6H820	Q6H820 oryza sativ
2	37	74.0	694	2 Q8EFS2	Q8EFS2 shewanella
3	37	74.0	1203	2 Q8S2E4	Q8S2E4 oryza sativ
4	37	74.0	1234	2 Q8GU81	Q8GU81 oryza sativ
5	36	72.0	402	2 Q62CX8	Q62CX8 burkholderi
6	36	72.0	402	2 Q63M18	Q63M18 burkholderi
7	36	72.0	663	2 Q8UA95	Q8UA95 agrobacteri
8	36	72.0	709	2 Q7CSK5	Q7CSK5 agrobacteri
9	36	72.0	723	2 Q8H034	Q8H034 oryza sativ
10	36	72.0	778	2 Q7MA36	Q7MA36 wolfinella s
11	36	72.0	1072	2 Q69X93	Q69X93 oryza sativ
12	35	70.0	143	2 Q69S82	Q69S82 human herpe
13	35	70.0	184	2 Q6AQ91	Q6AQ91 desulfotale
14	35	70.0	329	2 Q9RJ7	Q9RJ7 streptomyc
15	35	70.0	692	1 XJH3 YEAST	P40358 saccharomyc
16	35	70.0	696	2 Q8Y833	Q8Y833 listeria mo
17	35	70.0	1228	2 Q6MK31	Q6MK31 bdellovibri
18	35	70.0	6977	2 Q7R034	Q7R034 giardia lam
19	34	68.0	153	2 Q6NA42	Q6NA42 rhodospseud
20	34	68.0	231	2 Q9A213	Q9A213 caulobacter
21	34	68.0	279	1 THEU THEVU	P04072 thermoactin
22	34	68.0	322	2 Q6AH23	Q6AH23 leifsonia x
23	34	68.0	342	2 Q8ZSL1	Q8ZSL1 pyrobaculum
24	34	68.0	342	2 Q8ZXL8	Q8ZXL8 pyrobaculum
25	34	68.0	342	2 Q9LS05	Q9LS05 arabidopsis
26	34	68.0	344	2 Q9FV51	Q9FV51 arabidopsis
27	34	68.0	568	2 Q8P7L4	Q8P7L4 xanthomonas
28	34	68.0	568	2 Q8PIV6	Q8PIV6 xanthomonas
29	34	68.0	579	1 MTC1_BACST	P43423 bacillus st
30	34	68.0	579	2 Q9RQK2	Q9RQK2 bacillus st
31	34	68.0	589	2 Q7F1D1	Q7F1D1 oryza sativ

32 34 68.0 596 2 Q7QH89 Q7QH89 anopheles g
33 34 68.0 649 1 YAY3_SCHPO Q10211 schizosacch
34 34 68.0 827 2 Q6ZG00 Q6ZG00 oryza sativ
35 34 68.0 866 2 Q6FY30 Q6FY30 candida gla
36 34 68.0 874 2 Q67R60 Q67R60 symbiobacte
37 34 68.0 912 2 Q8ZWI9 Q8ZWI9 pyrobaculum
38 34 68.0 920 2 Q8ALN0 Q8ALN0 bacteroides
39 34 68.0 945 2 Q7EZJ3 Q7EZJ3 oryza sativ
40 34 68.0 956 2 Q84812 Q84812 chlamydia t
41 34 68.0 1206 2 Q8ZXP1 Q8ZXP1 pyrobaculum
42 34 68.0 2785 2 Q8ZVB9 Q8ZVB9 pyrobaculum
43 33 66.0 162 2 Q8Z129 Q8Z129 salmonella
44 33 66.0 162 2 Q8ZK37 Q8ZK37 salmonella
45 33 66.0 162 2 Q83SS1 Q83SS1 salmonella

ALIGNMENTS

RESULT 1

Q6H820 PRELIMINARY; PRT; 421 AA.
AC Q6H820;
DT 05-JUL-2004 (T-EMBLrel. 27, Created)
DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
DE GCN5-related N-acetyltransferase-like.
GN Name=QJ1297_C09.4;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzaceae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AP004087; BAD25129.1; -
DR GO; GO:0008080; F:N-acetyltransferase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR InterPro; IPR000182; GCN5acetyl trans.
DR InterPro; IPR000504; RNA_rec_mot.
DR Pfam; PF00583; Acetyltransf_1; 1.
DR PROSITE; PS00030; RRM_RNP_1; UNKNOWN_1.
KW Transferase.
SQ SEQUENCE 421 AA; 44979 MW; 7A9968BFFC673920 CRC64;

Query Match 74.0%; Score 37; DB 2; Length 421;
Best Local Similarity 80.0%; Pred. No. 69;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIATAARVLD 10
||:|||||
Db 288 ASIATAARALD 297

RESULT 2

Q8EFS2 PRELIMINARY; PRT; 694 AA.
AC Q8EFS2;
DT 01-MAR-2003 (T-EMBLrel. 23, Created)
DT 01-MAR-2003 (T-EMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Acetyl-CoA carboxylase, biotin carboxylase, putative.
GN OrderedLocusNames=SO1894;
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=70863;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MR-1;
RX MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;

```

RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
RA Read T.D., Eisen J.A., Seshadri R., Ward N.L., Methe B.A.,
RA Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.J.,
RA Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
RA Haft D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
RA White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,
RA Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,
RA Uterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA Venter J.C., Nealeon K.H., Frazer C.M.,
RA "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis.";
RL Nat. Biotechnol. 20:1118-1123 (2002).
DR EMBL; AE015632; AAN54946.1; -.
DR HSSP; P24182; 1DVI.
DR TIGR; SO1894; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001882; Biotin BS.
DR InterPro; IPR005482; Biotin_carb_C.
DR InterPro; IPR000889; Biotin_lipoY.
DR InterPro; IPR005481; CPase_L_N.
DR InterPro; IPR005479; Cphb synth_L_D2.
DR InterPro; IPR011053; Hybrid motif.
DR InterPro; IPR011054; Rudmnt_hyb motif.
DR Pfam; PF02785; Biotin_carb_C; 1.
DR Pfam; PF03664; Biotin_lipoY; 1.
DR Pfam; PF0289; CPase_L_chain; 1.
DR Pfam; PF02786; CPase_L_D2; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00866; CPASE_1; UNKNOWN_1.
DR PROSITE; PS00867; CPASE_2; UNKNOWN_1.
KW Biotin; Complete proteome.
SQ SEQUENCE 694 AA; 75656 MW; 05C4ECD8F03C998F CRC64;

Query Match 74.0%; Score 37; DB 2; Length 694;
Best Local Similarity 54.5%; Pred. No. 1.1e+02;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAAARVDY 11
Db 268 AAVAAKAIDY 278
|:||||:|
|:||||:|

RESULT 3
Q8S2E4 PRELIMINARY; PRT; 1203 AA.
AC Q8S2E4;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative P-glycoprotein.
GN Name=P002F10.15;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Sasaki T., Matsumoto T., Yamamoto K., Sakata K., Baba T., Katayose Y.,
RA Wu J., Niimura Y., Cheng Z., Nagamura Y., Antonio B.A., Kanamori H.,
RA Hosokawa S., Masukawa M., Arioka K., Chiden Y., Hayashi M.,
RA Okamoto M., Ando T., Aoki H., Arita K., Hamada M., Harada C.,
RA Hijishita S., Honda M., Ichikawa Y., Idonuma A., Iijima M., Ikeda M.,
RA Ikono M., Itoh S., Itoh Y., Itoh Y., Iwabuchi A., Kamiya K.,
RA Karsawa W., Katagiri S., Kikuta A., Kobayashi N., Kono I.,
RA Machita K., Machara T., Mizuno H., Mizubayashi T., Mukai Y.,
RA Nagasaki H., Nakashima M., Nakama Y., Nakamichi Y., Nakamura M.,
RA Namiki N., Negishi N., Ohta I., Ono N., Saji S., Sakai, K., Shibata M.,
RA Shimokawa T., Shomura A., Song J., Takazaki Y., Terasawa K., Tsuji K.,

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RA Waki K., Yamagata H., Yamane H., Yoshiki S., Yoshihara R., Yukawa K.,
RA Zhong H., Iwama H., Endo T., Ito H., Hahn J.H., Kim H.I., Eun M.Y.,
RA Yano M., Jiang J., Cojobori T.;
RT "The genome sequence and structure of rice chromosome 1.";
RL Nature 420:312-316 (2002).
CC -!- SMILARITY: Belongs to the ABC transporter family.
DR EMBL; AP003229; BAB89499.1; -.
DR HSSP; P08716; 1MT0.
DR Gramene; Q8S2E4; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0001166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011527; ABC_membrane_1.
DR InterPro; IPR001140; ABC_TM_transpt.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00664; ABC_membrane; 2.
DR Pfam; PF00005; ABC_tran; 2.
DR ProDom; PD000006; ABC_transporter; 2.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS0929; ABC_TM1F; 2.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 2.
KW ATP-binding.
SQ SEQUENCE 1203 AA; 131506 MW; B7838BDC1B5F19AA CRC64;

Query Match 74.0%; Score 37; DB 2; Length 1203;
Best Local Similarity 70.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAAARVLD 10
Db 330 ASVAATRLD 339
|:||||:|
|:||||:|

RESULT 4
Q8GU81 PRELIMINARY; PRT; 1234 AA.
AC Q8GU81;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE MDR-like ABC transporter.
GN Name=mdr17;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Jasinski M., Ducos E., Martinoia E., Boutry M.;
RT "The ATP-binding cassette transporters: structure, function and gene
RT family comparison between rice and Arabidopsis.";
RL Plant Physiol. 0:0-0(0).
RN [2]
RP SEQUENCE FROM N.A.
RA Ducos E.;
RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: Belongs to the ABC transporter family.
DR EMBL; AJ535055; CAD59577.1; -.
DR HSSP; P08716; 1MT0.
DR Gramene; Q8GU81; -.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0042626; F:ATPase activity, coupled to transmembrane m. . .; IEA.
DR GO; GO:0001166; F:nucleotide binding; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR011527; ABC_membrane_1.
DR InterPro; IPR001140; ABC_TM_transpt.

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DR InterPro; IPR003439; ABC_transporter.
 DR Pfam; PF00664; ABC_membrane; 2.
 DR Pfam; PF00005; ABC_tran; 2.
 DR ProDom; PD000006; ABC_transporter; 2.
 DR SMART; SM00382; AAA; 2.
 DR PROSITE; PS00929; ABC_TM1F; 2.
 DR PROSITE; PS02011; ABC_TRANSPORTER_1; 2.
 DR PROSITE; PS00893; ABC_TRANSPORTER_2; 2.
 KW ATP-binding.
 SQ SEQUENCE 1234 AA; 134571 MW; C5F9E9D75D28AC93 CRC64;

Query Match 74.0%; Score 37; DB 2; Length 1234;

Best Local Similarity 70.0%; Pred. No. 2e+02; Length 1234;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASIAAARVLD 10

Db 330 ASVAARILD 339

RESULT 5

ID Q62CX8 PRELIMINARY; PRT; 402 AA.
 AC Q62CX8;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Major facilitator superfamily protein.
 GN ORFNames=BMAA0712;
 OS Burkholderia mallei ATCC 23344.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia.
 OX NCBI_TaxID=243160;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 23344;
 RA Nierman W.C., Deshaizer D., Kim H.S., Tettelin H., Nelson K.E.,
 RA Feidibiyum T., Ulrich R.L., Rinning C.M., Brinkac L.M., Daugherty S.C.,
 RA Davidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S.,
 RA Gwinn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R.,
 RA Mohammad Y., Nelson W.C., Radune D., Romero C.M., Sarria S.,
 RA Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N.,
 RA Zhou L., Fraser C.M.;
 RT "Structural flexibility in the Burkholderia mallei genome."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).
 DR EMBL; CP000011; AAU46877.1; -.
 SQ SEQUENCE 402 AA; 41596 MW; 6FCA16BE0F4B18EA CRC64;

Query Match 72.0%; Score 36; DB 2; Length 402;

Best Local Similarity 70.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASIAAARVLD 10

Db 106 ATVAARLLD 115

RESULT 6

ID Q63M18 PRELIMINARY; PRT; 402 AA.
 AC Q63M18;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Putative transporter protein.
 GN ORFNames=BPSS0842;
 OS Burkholderia pseudomallei K96243.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
 OC Burkholderiaceae; Burkholderia.
 OX NCBI_TaxID=272560;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K96243;

RX PubMed=15377794;
 RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,
 RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
 RA Bentley S.D., Sebaihia M., Thomson N.R., Bason N., Beacham I.R.,
 RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
 RA Chillingworth T., Cronin A., Crosset B., Davis P., Deshaizer D.,
 RA Fellwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
 RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
 RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
 RA Songvilai S., Stevens K., Tumapa S., Vesaratchaveh M.,
 RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
 RT "Genomic plasticity of the causative agent of melioidosis,
 RT Burkholderia pseudomallei.";
 RL EMBL; BX571966; CAH38304.1; -.
 DR EMBL; BX571966; CAH38304.1; -.
 SQ SEQUENCE 402 AA; 41596 MW; 6FCA16BE0F4B18EA CRC64;

Query Match 72.0%; Score 36; DB 2; Length 402;

Best Local Similarity 70.0%; Pred. No. 1.1e+02;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASIAAARVLD 10

Db 106 ATVAARLLD 115

RESULT 7

ID Q8UA95 PRELIMINARY; PRT; 663 AA.
 AC Q8UA95;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE 3-methylcrotonyl-CoA carboxylase alpha subunit.
 GN Name=mccA; OrderedLocusNames=Atu3479;
 OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
 OX NCBI_TaxID=176299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Dupont;
 RA MEDLINE=1608550; PubMed=11743193; DOI=10.1126/science.1066804;
 RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
 RA Kutayvin T., Levy R., Li M.-J., McClelland E., Palmieri A.,
 RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Nester E.W.;
 RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
 RT C58.";
 RL Science 294:2317-2323(2001).
 DR EMBL; AE009278; AAL44292.1; -.
 DR PIR; A98299; A98299.
 DR PIR; AF2984; AF2984.
 DR HSSP; P24182; 1ENC.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0009374; F:biotin binding; IEA.
 DR GO; GO:0016874; F:ligase activity; IEA.
 DR GO; GO:0008152; P:metabolism; IEA.
 DR Pfam; PF02785; Biotin carb C; 1.
 DR Pfam; PF00364; Biotin_lipoyl; 1.
 DR Pfam; PF00289; CFSase_L_chain; 1.
 DR PROSITE; PS00188; BIOTIN; 1.
 DR PROSITE; PS00866; CFSASE_1; UNKNOWN_1.
 DR PROSITE; PS00867; CFSASE_2; UNKNOWN_1.
 KW Biotin; Complete proteome.
 SQ SEQUENCE 663 AA; 71187 MW; 2366201C5F36D292 CRC64;

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Query Match      72.0%; Score 36; DB 2; Length 663;
Best Local Similarity 63.6%; Pred. No. 1.7e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAAARVLDY 11
   | : ||||| : ||
Db 258 AATAAARAIDY 268

RESULT 8
Q7CSK5 PRELIMINARY; PRT; 709 AA.
AC Q7CSK5;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE AGR_L_2704p.
GN OrderedLocusNames=AGR_L_2704;
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
OX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Cereon;
RX MEDLINE=21608551; PubMed=11743194; DOI=10.1126/science.1066803;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
RA Qurrello B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
RA Houmlel K., Gordon J., Vaudin M., Iartchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gursion J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58."
RL Science 294:2323-2328 (2001).
DR EMBL; AE008334; AAK89915.1; -.
DR HSSP; P02905; 1BDO.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0009374; F:biotin binding; IEA.
DR GO; GO:0016874; F:ligase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR001882; Biotin BS.
DR InterPro; IPR005482; Biotin carb C.
DR InterPro; IPR005481; CPase_I_N.
DR InterPro; IPR005479; Cph synth_L_D2.
DR InterPro; IPR011053; Hybrid motif.
DR InterPro; IPR011054; Rudmt_hyb_motif.
DR Pfam; PF02785; Biotin carb C; 1.
DR Pfam; PF00364; Biotin lipoyl; 1.
DR Pfam; PF00289; CPase_L_chain; 1.
DR PROSITE; PS00188; BIOTIN; 1.
DR PROSITE; PS00866; CPASE_1; UNKNOWN_1.
DR PROSITE; PS00867; CPASE_2; UNKNOWN_1.
KW Biotin.
SQ SEQUENCE 709 AA; 76278 MW; 1F43A1F11919EF00 CRC64;

Query Match      72.0%; Score 36; DB 2; Length 709;
Best Local Similarity 63.6%; Pred. No. 1.8e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAAARVLDY 11
   | : ||||| : ||
Db 304 AATAAARAIDY 314

RESULT 9
Q8H034 PRELIMINARY; PRT; 723 AA.
AC Q8H034;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

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DE Hypothetical protein QJ1172F09.9.
GN Name=QJ1172F09.9;
OS Oryza sativa (japonica cultivar-group).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=39947;
RN [1]
RP SEQUENCE FROM N.A.
RA Wing R.A., Yu Y., Soderlund C., Kim H.-R., Rambo T., Currie J.,
RA Collura K., McCombie D.W.R., de la Bastide M., Spiegel L., Preston R.,
RA Kirchoff K., Kuit K., Nascimento L., Zutavern T., Balija V., Bell M.,
RA Baker J., Santos L., Miller B., Katzenberger F., Muller S., King L.,
RA Yang C., O'Shaughnessy A., Palmer L., Dedhia N.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC119796; AAO17354.1; -.
DR Gramene; Q8H034; -.
DR InterPro; IPR008938; ARM.
KW Hypothetical protein.
SQ SEQUENCE 723 AA; 78613 MW; 3FD842215E6ED1FD CRC64;

Query Match      72.0%; Score 36; DB 2; Length 723;
Best Local Similarity 80.0%; Pred. No. 1.9e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 ASIAAARVLD 10
   | : ||||| |
Db 616 ASLAARVTD 625

RESULT 10
Q7MA36 PRELIMINARY; PRT; 778 AA.
ID Q7MA36
AC Q7MA36;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE FLAGELLAR FUNCTIONAL PROTEIN.
GN Name=PFLA; OrderedLocusNames=WS0490;
OS Wolinella succinogenes.
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Wolinella.
OX NCBI_TaxID=844;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSMZ 1740;
RX MEDLINE=22882897; PubMed=14500908; DOI=10.1073/pnas.1932838100;
RA Baar C., Eppinger M., Raddatz G., Simon J., Lanz C., Klimmek O.,
RA Nandakumar R., Gross R., Rosinus A., Keller H., Jagtap P., Linke B.,
RA Meyer F., Lederer H., Schuster S.C.;
RT "Complete genome sequence and analysis of Wolinella succinogenes."
RL Proc. Natl. Acad. Sci. U.S.A. 100:11690-11695 (2003).
DR EMBL; BX571658; CAE09628.1; -.
DR GO; GO:0019861; C:flagellum; IEA.
DR InterPro; IPR008940; Prenyl_trans.
DR InterPro; IPR001440; TPR.
DR InterPro; IPR008941; TPR-like.
DR Pfam; PF00515; TPR_1; 1.
DR PROSITE; PS50293; TPR_REGION; 1.
KW Complete proteome; Flagellum.
SQ SEQUENCE 778 AA; 89775 MW; 3E2F992CE949C27E CRC64;

Query Match      72.0%; Score 36; DB 2; Length 778;
Best Local Similarity 63.6%; Pred. No. 2e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 ASIAAARVLDY 11
   | : ||||| : ||
Db 322 ASLAARVLDY 332

RESULT 11
Q69X93

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"A transforming fragment within the direct repeat region of human herpesvirus type 6 that transactivates HIV-1.";
Oncogene 9:1167-1175(1994).
[2]
RN RN
RP SEQUENCE FROM N.A.
RA Thompson J.T.,
RL Submitted (JUN-1993) to the EMBL/GenBank/DDBJ databases.
DR EMBL; X73675; CAA52028.1; -.
DR PIR; S43071; S43071.
SQ SEQUENCE 143 AA; 13317 MW; BDF78898C3D31734 CRC64;

Query Match 70.0%; Score 35; DB 2; Length 143;
Best Local Similarity 88.9%; Pred.No. 63;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASIAAARVLD 9
||:|||||
DB 7 ASLAARVLD 15

RESULT 13
Q6AQ91 PRELIMINARY; PRT; 184 AA.
AC Q6AQ91
DT 25-OCT-2004 (TtEMBLrel. 28, Created)
DT 25-OCT-2004 (TtEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TtEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
GN OrderedLocusNames=DP0753;
OS Desulfotalea psychrophila.
OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfobacteriales;
OC Desulfobulbacae; Desulfotalea.
OX NCBI_TaxID=84980;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LSv54 / DSM 12343;
RX PubMed=15305914;
RA Rabus R., Ruepp A., Frickay T., Rattei T., Fartmann B., Stark M.,
RA Bauer M., Zibat A., Lombardot T., Becker I., Amann J., Gellner K.,
RA Teeling H., Leuschner W.D., Gloeckner F.-O., Lupas A.N., Amann R.,
RA Klenk H.-P.;
RT "The genome of Desulfotalea psychrophila, a sulfate-reducing bacterium from permanently cold Arctic sediments.";
RL Environ. Microbiol. 6:887-902(2004).
DR EMBL; CR522870; CAG35482.1; -.
KW Complete proteome.
SQ SEQUENCE 184 AA; 20792 MW; 8D9DCB5EDFAA60AF CRC64;

Query Match 70.0%; Score 35; DB 2; Length 184;
Best Local Similarity 80.0%; Pred.No. 81;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 ASIAAARVLD 10
||:|||||
DB 99 ASLAARVLDN 108

RESULT 14
Q9RJR7 PRELIMINARY; PRT; 329 AA.
AC Q9RJR7
DT 01-MAY-2000 (TtEMBLrel. 13, Created)
DT 01-MAY-2000 (TtEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TtEMBLrel. 25, Last annotation update)
DE Putative zinc-binding oxidoreductase.
GN ORFNames=SCF51.18;
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinomycetidae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;

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RX MEDLINE=21996410; PubMed=12000953; DOI=10.1038/417141a;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidaigo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L.D., Oliver K., O'Neill S.,
RA Rabinowitch E., Rajandream M.A., Rutherford K.M., Rutter S.,
RA Seger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J.R., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939105; CAB59716.1; -.
DR HSSP; O8L3C8; 11YZ.
DR GO; GO:0004024; F:alcohol dehydrogenase activity, zinc-dependent; IEA.
DR GO; GO:0008270; F:zinc ion binding; IEA.
DR InterPro; IPR002085; Adh_zn family.
DR InterPro; IPR011032; GroES like.
DR Pfam; PF00107; ADH_zinc_N; 1.
KW Complete proteome.
SQ SEQUENCE 329 AA; 34155 MW; 5DCAD4FB174FD042 CRC64;

Query Match 70.0%; Score 35; DB 2; Length 329;
Best Local Similarity 70.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 SIAAARVLDY 11
DB 189 SLGAHVLDY 198

RESULT 15
YOH3 YEAST
ID YOH3 YEAST STANDARD; PRT; 692 AA.
AC P40358;
DC 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Hypothetical 80.4 kDa protein in SMC3-MRPL8 intergenic region.
GN OrderedLocustNames=YUL073W; ORFNames=YJ083, HRC558;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Rose M., Koetter P., Entian K.D.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Sor F.J.;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 135-692 FROM N.A.
RC STRAIN=S288c;
RX MEDLINE=95282514; PubMed=7762302;
RA Vandenbol M., Durand P., Dion C., Portetelle D., Hilger F.;
RT "Sequence of a 17.1 kb DNA fragment from chromosome X of Saccharomyces
RT cerevisiae includes the mitochondrial ribosomal protein L8.";
RL Yeast 11:57-60(1995).
CC -!- SIMILARITY: Contains 1 J domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z49348; CAA89365.1; -.

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DR EMBL; X88851; CAA61312.1; -.
DR EMBL; Z34288; CAA84049.1; -.
DR PIR; S56849; S56849.
DR HSSP; P08622; 1BQZ.
DR GerMOnline; 141687; -.
DR SGD; S000003609; JEM1.
DR GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR GO; GO:0000300; C:peripheral to membrane of membrane fraction; IDA.
DR GO; GO:0003767; F:co-chaperone activity; IGI.
DR GO; GO:0000742; P:karyogamy during conjugation with cellular . . .; IGI.
DR GO; GO:0006457; P:protein folding; IGI.
DR InterPro; IPR001623; DnaJ_N.
DR Pfam; PF00226; DnaJ; 1.
DR SMART; SM00271; DnaJ; 1.
DR PROSITE; PS00636; DnaJ_1; FALSE_NEG.
DR PROSITE; PS50076; DnaJ_2; 1.
KW Hypothetical protein.
FT DOMAIN 560 569 Poly-Gln.
FT DOMAIN 585 655 J-domain.
SQ SEQUENCE 692 AA; 80381 MW; 9F612DD16B66981B CRC64;

Query Match 70.0%; Score 35; DB 1; Length 692;
Best Local Similarity 70.0%; Pred. No. 2.9e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SIAAARVLDY 11
DB 245 SIAAAIILDY 254

Search completed: October 14, 2005, 16:19:53
Job time : 75.2188 secs

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RESULT 2
US-09-383-667-19
; Sequence 19, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hass, Philip S.
; APPLICANT: Justice, J. Kevin
; APPLICANT: Kirchhofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
FILE REFERENCE: P1661R2

; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 19
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-19

Query Match 92.0%; Score 46; DB 4; Length 11;
Best Local Similarity 90.9%; Pred. No. 0.0013;
Matches 10; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASIAAARVLDY 11
Db 1 ASIAAGRVLDY 11

RESULT 3
US-09-342-648-2
; Sequence 2, Application US/09342648
; Patent No. 6248584
; GENERAL INFORMATION:
; APPLICANT: Cahoon, Rebecca E.
; APPLICANT: Odell, Joan
; APPLICANT: Rafalski, Antoni
; TITLE OF INVENTION: Transcription Coactivators
; FILE REFERENCE: BB-1169-B
; CURRENT APPLICATION NUMBER: US/09/342,648
; CURRENT FILING DATE: 1999-06-29
; EARLIER APPLICATION NUMBER: 60/092,659
; EARLIER FILING DATE: July 13, 1998
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 2
; LENGTH: 755
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (179)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (185)
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (241)
US-09-342-648-2

Query Match 72.0%; Score 36; DB 3; Length 755;
Best Local Similarity 72.7%; Pred. No. 30;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 ASIAAARVLDY 11
Db 240 AXIADTRVLDY 250

RESULT 4
US-08-865-203-6
; Sequence 6, Application US/08865203
; Patent No. 5935815
; GENERAL INFORMATION:
; APPLICANT: van de Ven, Willem Jan Marie
; APPLICANT: van den Ouweland, Anna Maria Wilhelmina
; APPLICANT: Van Duijnhooven, Johannes Lambertus Petrus
; APPLICANT: Robroek, Antonius Johannes Maria
; APPLICANT: Koning, Piet Nico Maria
; TITLE OF INVENTION: Pharmaceutical Composition Having An

; TITLE OF INVENTION: Endoproteolytic Activity; A Process for
; TITLE OF INVENTION: Endoproteolytically Processing (Precursor)
; TITLE OF INVENTION: Proteins And For The (Micro)Biological
; TITLE OF INVENTION: Production Of Proteins
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOFFMANN & BARON, LLP
; STREET: 350 Jericho Turnpike
; CITY: Jericho
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11753
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,203
; FILING DATE: 29-MAY-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Tran, Jessica H.
; REGISTRATION NUMBER: 40,846
; REFERENCE/DOCKET NUMBER: 294-41 DIV II
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 822-3550
; TELEFAX: (516) 822-3582
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 278 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-865-203-6
Query Match 68.0%; Score 34; DB 2; Length 278;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 ASIAAARVLD 10
Db 96 ASILAVRVLD 105
RESULT 5
US-07-849-420-6
; Sequence 6, Application US/07849420
; Patent No. 5989856
; GENERAL INFORMATION:
; APPLICANT: van de Ven, Willem Jan Marie
; APPLICANT: van den Ouweland, Anna Maria Wilhelmina
; APPLICANT: Van Duijnhooven, Johannes Lambertus Petrus
; APPLICANT: Robroek, Antonius Johannes Maria
; APPLICANT: Koning, Piet Nico Maria
; TITLE OF INVENTION: Pharmaceutical Composition Having An
; TITLE OF INVENTION: Endoproteolytic Activity; A Process for
; TITLE OF INVENTION: Endoproteolytically Processing (Precursor)
; TITLE OF INVENTION: Proteins And For The (Micro)Biological
; TITLE OF INVENTION: Production Of Proteins
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/849,420
; FILING DATE: 19920624
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, Thomas F.
; REGISTRATION NUMBER: 16,579
; REFERENCE/DOCKET NUMBER: 2805/41413
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 977-9550
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 278 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-849-420-6

Query Match 68.0%; Score 34; DB 2; Length 278;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAAARVLD 10
   |||||
Db 96 ASILAVRVLD 105

RESULT 6
US-09-253-854-6
; Sequence 6, Application US/09253854
; Patent No. 6132717
; GENERAL INFORMATION:
; APPLICANT: van de Ven, Willem Jan Marie;
; APPLICANT: van den Ouweland, Anna Maria Wilhelmina;
; APPLICANT: Van Duijnhoven, Johannes Lambertus Petrus;
; APPLICANT: Robroek, Antonius Johannes Maria;
; APPLICANT: Koning, Piet Nico Maria
; TITLE OF INVENTION: Pharmaceutical Composition Having An
; TITLE OF INVENTION: Endoproteolytic Activity; A process for
; TITLE OF INVENTION: Endoproteolytically Processing (precursor)
; TITLE OF INVENTION: Proteins And For The (Micro)Biological
; TITLE OF INVENTION: Production Of Proteins
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HOFFMANN & BARON, LLP
; STREET: 350 Jericho Turnpike
; CITY: Jericho
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11753
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/253,854
; FILING DATE: Unassigned
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Tran, Jessica H.
; REGISTRATION NUMBER: 40,846
; REFERENCE/DOCKET NUMBER: 294-41 DIV II/CON
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 822-3550
; TELEFAX: (516) 822-3582
; TELEX:
; INFORMATION FOR SEQ ID NO: 6:
; LENGTH: 279
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; SEQUENCE CHARACTERISTICS:
; LENGTH: 278 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-253-854-6

Query Match 68.0%; Score 34; DB 3; Length 278;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAAARVLD 10
   |||||
Db 96 ASILAVRVLD 105

RESULT 7
US-08-955-424-6
; Sequence 6, Application US/08955424
; Patent No. 6274365
; GENERAL INFORMATION:
; APPLICANT: Van de Ven, Willem Jan Marie
; APPLICANT: Van de Ouweland, Anna Maria Wilhelmina
; APPLICANT: Van Duijnhoven, Johannes Lambertus Petrus
; APPLICANT: Koning, Piet Nico Maria
; APPLICANT: Robroek, Antonius Johannes Maria
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITION HAVING AN ENDOPROTEOLYTIC
; TITLE OF INVENTION: ACTIVITY; A PROCESS FOR ENDOPROTEOLYTICALLY PROCESSING
; TITLE OF INVENTION: (PRECURSOR) PROTEINS AND FOR THE (MICRO) BIOLOGICAL
; TITLE OF INVENTION: PRODUCTION OF PROTEINS
; FILE REFERENCE: SEQUENCE LISTINGS 1-12 294-41 DIV/FWC
; CURRENT APPLICATION NUMBER: US/08/955,424
; CURRENT FILING DATE: 1997-10-22
; EARLIER APPLICATION NUMBER: 08/568,152
; EARLIER FILING DATE: 1995-06-12
; EARLIER APPLICATION NUMBER: 07/849,420
; EARLIER FILING DATE: 1992-06-24
; EARLIER APPLICATION NUMBER: PCT/NL90/00151
; EARLIER FILING DATE: 1990-10-21
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 278
; TYPE: PRT
; ORGANISM: Thermoactinomyces vulgaris
; US-08-955-424-6

Query Match 68.0%; Score 34; DB 3; Length 278;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAAARVLD 10
   |||||
Db 96 ASILAVRVLD 105

RESULT 8
US-09-135-658-4
; Sequence 4, Application US/09135658
; Patent No. 5972683
; GENERAL INFORMATION:
; APPLICANT: TSAI, Ying-Chieh
; TITLE OF INVENTION: MUTANT TYPE SUBTILISIN YAB AND ITS APPLICATION
; FILE REFERENCE: 6653-011-999
; CURRENT APPLICATION NUMBER: US/09/135,658
; CURRENT FILING DATE: 1998-08-18
; EARLIER APPLICATION NUMBER: 86112766
; EARLIER FILING DATE: 1997-09-04
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.0 - beta
; SEQ ID NO 4
; LENGTH: 279
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; TYPE: PRT
; ORGANISM: Bacillus subtilis
US-09-135-658-4

Query Match      68.0%; Score 34; DB 2; Length 279;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 ASIAARVLD 10
Db      96 ASILAVRVL 105

RESULT 9
US-09-512-251A-6
; Sequence 6, Application US/09512251A
; Patent No. 6555355
; GENERAL INFORMATION:
; APPLICANT: Hansen, Peter
; APPLICANT: Bauditz, Peter
; APPLICANT: Mikkelsen, Frank
; APPLICANT: Andersen, Kim
; TITLE OF INVENTION: Protease Variants and Compositions
; FILE REFERENCE: 5349.204-US
; CURRENT APPLICATION NUMBER: US/09/512,251A
; CURRENT FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Bacillus
US-09-512-251A-6

Query Match      68.0%; Score 34; DB 4; Length 279;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 ASIAARVLD 10
Db      96 ASILAVRVL 105

RESULT 10
US-09-515-150A-6
; Sequence 6, Application US/09515150A
; Patent No. 6558938
; GENERAL INFORMATION:
; APPLICANT: Hansen, Peter
; APPLICANT: Bauditz, Peter
; APPLICANT: Mikkelsen, Frank
; APPLICANT: Andersen, Kim
; TITLE OF INVENTION: Protease Variants and Compositions
; FILE REFERENCE: 5348.204-US
; CURRENT APPLICATION NUMBER: US/09/515,150A
; CURRENT FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Bacillus
US-09-515-150A-6

Query Match      68.0%; Score 34; DB 4; Length 279;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 ASIAARVLD 10
Db      96 ASILAVRVL 105

RESULT 11
US-09-196-281-9
; Sequence 9, Application US/09196281A
; Patent No. 6605458
; GENERAL INFORMATION:
; APPLICANT: Hansen, Peter K.
; APPLICANT: Bauditz, Peter
; APPLICANT: Mikkelsen, Frank
; TITLE OF INVENTION: Protease Variants and Compositions
; FILE REFERENCE: 5435.200-US
; CURRENT APPLICATION NUMBER: US/09/196,281A
; CURRENT FILING DATE: 1998-11-19
; EARLIER APPLICATION NUMBER: 1332/97
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 279
; TYPE: PRT
; ORGANISM: Bacillus
US-09-196-281-9

Query Match      68.0%; Score 34; DB 4; Length 279;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 ASIAARVLD 10
Db      96 ASILAVRVL 105

RESULT 12
5472855-6
; Patent No. 5472855
; TITLE OF INVENTION: SUBSTRATE ASSISTED CATALYSIS
; NUMBER OF SEQUENCES: 31
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/287,964
; FILING DATE: 22-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 90,902
; FILING DATE: 12-JUL-1993
; APPLICATION NUMBER: 823,039
; FILING DATE: 14-JAN-1992
; APPLICATION NUMBER: 35,652
; FILING DATE: 06-APR-1987
; APPLICATION NUMBER: 334,081
; FILING DATE: 04-APR-1989
; APPLICATION NUMBER: 127,134
; APPLICATION NUMBER: 846,627
; FILING DATE: 01-DEC-1987
; APPLICATION NUMBER: 858,594
; FILING DATE: 01-APR-1986
; APPLICATION NUMBER: 858,594
; FILING DATE: 30-APR-1986
; APPLICATION NUMBER: 614,612
; FILING DATE: 29-MAY-1984
; APPLICATION NUMBER: 614,615
; FILING DATE: 29-MAY-1984
; APPLICATION NUMBER: 614,617
; FILING DATE: 29-MAY-1984
; APPLICATION NUMBER: 614,491
; FILING DATE: 29-MAY-1984
; SEQ ID NO: 6
; LENGTH: 279
5472855-6

Query Match      68.0%; Score 34; DB 6; Length 279;
Best Local Similarity 80.0%; Pred. No. 25;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 ASIAARVLD 10
Db      96 ASILAVRVL 105
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Db          96 ASILAVRVD 105

RESULT 13
5472855-6
;PATENT NO. 5472855
;APPLICANT: CARTER, PAUL J.; WELLS, JAMES A.
;TITLE OF INVENTION: SUBSTRATE ASSISTED CATALYSIS
;NUMBER OF SEQUENCES: 31
;CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/08/287,964
;  FILING DATE: 22-SEP-1994
;PRIOR APPLICATION DATA:
;  APPLICATION NUMBER: 90,902
;  FILING DATE: 12-JUL-1993
;  APPLICATION NUMBER: 823,039
;  FILING DATE: 14-JAN-1992
;  APPLICATION NUMBER: 35,652
;  FILING DATE: 06-APR-1987
;  APPLICATION NUMBER: 334,081
;  FILING DATE: 04-APR-1989
;  APPLICATION NUMBER: 127,134
;  FILING DATE: 01-DEC-1987
;  APPLICATION NUMBER: 846,627
;  FILING DATE: 01-APR-1986
;  APPLICATION NUMBER: 858,594
;  FILING DATE: 30-APR-1986
;  APPLICATION NUMBER: 614,612
;  FILING DATE: 29-MAY-1984
;  APPLICATION NUMBER: 614,615
;  FILING DATE: 29-MAY-1984
;  APPLICATION NUMBER: 614,617
;  FILING DATE: 29-MAY-1984
;  APPLICATION NUMBER: 614,491
;  FILING DATE: 29-MAY-1984
;SEQ ID NO:6:
;  LENGTH: 279
5472855-6

Query Match          68.0%; Score 34; DB 6; Length 279;
Best Local Similarity 80.0%; Pred. No. 25;
Matches      8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy          1 ASIAARVLD 10
      |||||
Db          96 ASILAVRVD 105

RESULT 14
US-09-698-286A-10
; Sequence 10, Application US/09698286A
; Patent No. 667442
; GENERAL INFORMATION:
; APPLICANT: University of Kentucky Research Foundation
; TITLE OF INVENTION: Human REV1 Gene and Protein As Diagnostic, Preventive, and Therap
; FILE REFERENCE: 050229-0247
; CURRENT APPLICATION NUMBER: US/09/698,286A
; CURRENT FILING DATE: 2000-10-30
; PRIOR APPLICATION NUMBER: 60/162,140
; PRIOR FILING DATE: 1999-10-29
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 85
; TYPE: PRT
; ORGANISM: C. elegans, A. thaliana, S. cerevisiae, S. pombe and H. sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (17)..(22)
; OTHER INFORMATION: Gap in alignment
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (50)..(60)
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; OTHER INFORMATION: Gap in alignment
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (30)..(33)
; OTHER INFORMATION: Gap in alignment
US-09-698-286A-10

Query Match          66.0%; Score 33; DB 4; Length 85;
Best Local Similarity 70.0%; Pred. No. 9.8;
Matches      7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy          2 SIAAARVLDY 11
      |||||
Db          71 SIAAGKPLDY 80

RESULT 15
US-09-710-279-622
; Sequence 622, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/09/710,279
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn ver. 2.1
; SEQ ID NO 622
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-09-710-279-622

Query Match          66.0%; Score 33; DB 4; Length 194;
Best Local Similarity 60.0%; Pred. No. 26;
Matches      6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy          2 SIAAARVLDY 11
      |||||
Db          106 NVASASVLDY 115

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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:20:10 ; Search time 78.2031 Seconds
(without alignments)
58.615 Million cell updates/sec

Title: US-10-614-959-12
Perfect score: 50
Sequence: 1 ASTAARVLDY 11

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Maximum Match 100%
Listing first 45 summaries

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- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
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- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
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- 18: /cgn2_6/ptodata/2/pubpaa/US10F_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	40	80.0	183	US-10-425-115-369042 Sequence 369042,
2	37	74.0	408	US-10-389-566-831 Sequence 831, App
3	37	74.0	573	US-10-425-114-45544 Sequence 45544, A
4	37	74.0	573	US-10-425-115-208229 Sequence 208229,
5	37	74.0	694	US-10-425-115-208239 Sequence 208239,
6	37	74.0	1203	US-10-437-963-120758 Sequence 120758,
7	36	72.0	652	US-10-369-493-14688 Sequence 14688, A
8	36	72.0	652	US-10-369-493-15165 Sequence 15165, A
9	36	72.0	655	US-10-369-493-14406 Sequence 14406, A
10	36	72.0	656	US-10-369-493-11635 Sequence 11635, A
11	36	72.0	1064	US-10-437-963-189048 Sequence 189048,

12	35	70.0	45	16	US-10-437-963-201347	Sequence 201347,
13	35	70.0	107	16	US-10-437-963-175236	Sequence 175236,
14	34	68.0	198	16	US-10-767-701-38892	Sequence 38892, A
15	34	68.0	231	15	US-10-369-493-17091	Sequence 17091, A
16	34	68.0	279	14	US-10-336-324-6	Sequence 6, Appli
17	34	68.0	279	14	US-10-403-105-9	Sequence 9, Appli
18	34	68.0	341	16	US-10-425-115-353435	Sequence 353435,
19	34	68.0	642	16	US-10-767-701-45651	Sequence 45651, A
20	34	68.0	671	15	US-10-369-493-7093	Sequence 7093, Ap
21	34	68.0	674	15	US-10-369-493-4338	Sequence 4338, Ap
22	34	68.0	691	15	US-10-425-114-70274	Sequence 70274, A
23	34	68.0	827	16	US-10-437-963-146706	Sequence 146706,
24	34	68.0	1000	16	US-10-437-963-122779	Sequence 122779,
25	33	66.0	204	14	US-10-238-075-276	Sequence 276, App
26	33	66.0	223	18	US-10-724-972A-5583	Sequence 5583, Ap
27	33	66.0	274	14	US-10-032-585-7697	Sequence 7697, Ap
28	33	66.0	299	15	US-10-425-114-40808	Sequence 40808, A
29	33	66.0	331	14	US-10-156-761-8701	Sequence 8701, Ap
30	33	66.0	358	15	US-10-282-122A-62045	Sequence 62045, A
31	33	66.0	358	15	US-10-282-122A-63923	Sequence 63923, A
32	33	66.0	367	15	US-10-282-122A-62857	Sequence 62857, A
33	33	66.0	367	15	US-10-282-122A-64830	Sequence 64830, A
34	33	66.0	371	20	US-11-058-046-5	Sequence 5, Appli
35	33	66.0	402	15	US-10-627-476-508	Sequence 508, App
36	33	66.0	449	9	US-09-738-626-6555	Sequence 6555, App
37	33	66.0	453	15	US-10-369-493-21054	Sequence 21054, A
38	33	66.0	466	16	US-10-437-963-136788	Sequence 136788,
39	33	66.0	469	15	US-10-417-700A-49	Sequence 49, Appl
40	33	66.0	509	15	US-10-282-122A-77407	Sequence 77407, A
41	33	66.0	670	15	US-10-369-493-11847	Sequence 11847, A
42	33	66.0	862	16	US-10-425-115-189243	Sequence 189243,
43	33	66.0	867	15	US-10-282-122A-63141	Sequence 63141, A
44	33	66.0	1958	14	US-10-152-886-53	Sequence 53, Appl
45	33	66.0	1958	20	US-11-053-576-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1

US-10-425-115-369042
; Sequence 369042, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 369042
; LENGTH: 183
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(183)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_99740C.1.pep
US-10-425-115-369042

Query Match 80.0%; Score 40; DB 16; Length 183;
Best Local Similarity 90.0%; Pred. No. 7.9;
Matches 9; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 SIAARVLDY 11
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Db 91 SIAARVLDY 100

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RESULT 2
US-10-389-566-831
; Sequence 831, Application US/10389566
; Publication No. US20040025202A1
; GENERAL INFORMATION:
; APPLICANT: Monsanto Technology, LLC
; APPLICANT: Laurie, Cathy C
; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
; FILE REFERENCE: 38-77(52900)D
; CURRENT APPLICATION NUMBER: US/10/389,566
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: US 60/365,301
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/391,786
; PRIOR FILING DATE: 2002-06-25
; PRIOR APPLICATION NUMBER: US 60/392,018
; PRIOR FILING DATE: 2002-06-26
; NUMBER OF SEQ ID NOS: 2459
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 831
; LENGTH: 408
; TYPE: PRT
; ORGANISM: Oryza sativa
; NAME/KEY: misc feature
; LOCATION: (103)..(104)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-389-566-831

Query Match          74.0%; Score 37; DB 15; Length 408;
Best Local Similarity 80.0%; Pred. No. 73;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASIAAARVLD 10
|:|:|:|:|
Db 275 ASLAARALD 284

RESULT 3
US-10-425-114-45544
; Sequence 45544, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 45544
; LENGTH: 573
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700800359_FLI.pap
US-10-425-114-45544

Query Match          74.0%; Score 37; DB 15; Length 573;
Best Local Similarity 72.7%; Pred. No. 1e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAAARVLDY 11
|:|:|:|:|
Db 58 ANIADTRVLDY 68
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RESULT 4
US-10-425-115-208229
; Sequence 208229, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 208229
; LENGTH: 573
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_121499C.1.pap
US-10-425-115-208229

Query Match          74.0%; Score 37; DB 16; Length 573;
Best Local Similarity 72.7%; Pred. No. 1e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAAARVLDY 11
|:|:|:|:|
Db 58 ANIADTRVLDY 68

RESULT 5
US-10-425-115-208239
; Sequence 208239, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 208239
; LENGTH: 694
; TYPE: PRT
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_121507C.1.pap
US-10-425-115-208239

Query Match          74.0%; Score 37; DB 16; Length 694;
Best Local Similarity 72.7%; Pred. No. 1.3e+02;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAAARVLDY 11
|:|:|:|:|
Db 179 ANIADTRVLDY 189

RESULT 6
US-10-437-963-120758
; Sequence 120758, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
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; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 120758
; LENGTH: 1203
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_2384C.1.pep
US-10-437-963-120758

Query Match      74.0%; Score 37; DB 16; Length 1203;
Best Local Similarity 70.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 ASIAAARVLD 10
Db      330 ASVAATRI 339
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      ||:|||||:|

RESULT 7
US-10-369-493-14688
; Sequence 14688, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 14688
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14688

Query Match      72.0%; Score 36; DB 15; Length 652;
Best Local Similarity 63.6%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 ASIAAARVLDY 11
Db      255 AATAAARVDY 265
      |:|||||:|
      |:|||||:|

RESULT 8
US-10-369-493-15165
; Sequence 15165, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
```

```
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 15165
; LENGTH: 652
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-15165

Query Match      72.0%; Score 36; DB 15; Length 652;
Best Local Similarity 63.6%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 ASIAAARVLDY 11
Db      255 AATAAARVDY 265
      |:|||||:|
      |:|||||:|

RESULT 9
US-10-369-493-14406
; Sequence 14406, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 14406
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-14406

Query Match      72.0%; Score 36; DB 15; Length 655;
Best Local Similarity 63.6%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy      1 ASIAAARVLDY 11
Db      255 AATAAARVDY 265
      |:|||||:|
      |:|||||:|

RESULT 10
US-10-369-493-11635
; Sequence 11635, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2003-02-28
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 11635
```

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; LENGTH: 656
; TYPE: PRT
; ORGANISM: Agrobacterium tumefaciens
US-10-369-493-11635

Query Match      72.0%; Score 36; DB 15; Length 656;
Best Local Similarity 63.6%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 ASIAAARVLDY 11
   |:|||||:
Db 255 AATAARAIDY 265

RESULT 11
US-10-437-963-189048
; Sequence 189048, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 189048
; LENGTH: 1064
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_85594C.1.pep
US-10-437-963-189048

Query Match      72.0%; Score 36; DB 16; Length 1064;
Best Local Similarity 80.0%; Pred. No. 3.2e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASIAAARVLD 10
   |:|||||:
Db 116 ASLAARVLD 125

RESULT 12
US-10-437-963-201347
; Sequence 201347, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 201347
; LENGTH: 45
; TYPE: PRT
; ORGANISM: Oryza sativa
```

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; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_96731C.1.pep
US-10-437-963-201347

Query Match      70.0%; Score 35; DB 16; Length 45;
Best Local Similarity 88.9%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 SIAAARVLD 10
   |:|||||:
Db 16 SIATARVLD 24

RESULT 13
US-10-437-963-175236
; Sequence 175236, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 175236
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)-(107)
; OTHER INFORMATION: unsure at all Xaa locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_73100C.1.pep
US-10-437-963-175236

Query Match      70.0%; Score 35; DB 16; Length 107;
Best Local Similarity 80.0%; Pred. No. 45;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASIAAARVLD 10
   |:|||||:
Db 34 ASLAARVSD 43

RESULT 14
US-10-767-701-38892
; Sequence 38892, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
; SEQ ID NO 38892
; LENGTH: 198
; TYPE: PRT
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: SORBI-28MAY03-C77436_1.pep
```

US-10-767-701-38892

Query Match 68.0%; Score 34; DB 16; Length 198;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 AARVLDY 11

Db 114 AARVLDY 120

RESULT 15

US-10-369-493-17091
; Sequence 17091, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 17091
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Caulobacter crescentus
US-10-369-493-17091

Query Match 68.0%; Score 34; DB 15; Length 231;
Best Local Similarity 80.0%; Pred. No. 1.6e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASIAAARVLD 10

Db 100 ATIAAARKLD 109

Search completed: October 14, 2005, 17:00:43
Job time : 79.2031 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 14, 2005, 15:51:19 ; Search time 99.9375 Seconds
(without alignments)
50.310 Million cell updates/sec

Title: US-10-614-959-13
Perfect score: 66
Sequence: 1 SGSTSNIGNNYVS 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	100.0	13	3 AAY79071	Anti-fact
2	66	100.0	109	4 AAU02544	Anti-adip
3	66	100.0	110	4 AAU02558	Anti-adip
4	66	100.0	110	4 AAU02612	Anti-adip
5	66	100.0	110	4 AAU02627	Anti-adip
6	66	100.0	110	4 AAU02629	Anti-adip
7	66	100.0	111	4 AAU02542	Anti-adip
8	66	100.0	111	4 AAU02551	Anti-adip
9	66	100.0	240	5 ABP45887	Human Bly
10	66	100.0	240	7 ADG96714	Single ch
11	66	100.0	242	8 ADG34301	Neurokini
12	66	100.0	242	8 ADG34317	Neurokini
13	66	100.0	243	5 ABP45916	Human Bly
14	66	100.0	243	6 AAO31147	Human CM0
15	66	100.0	243	7 ADG96743	Single ch
16	66	100.0	243	8 ADG34310	Neurokini
17	66	100.0	243	8 ADG34306	Neurokini
18	66	100.0	244	8 ADG34303	Neurokini
19	66	100.0	245	5 ABP45915	Human Bly
20	66	100.0	245	7 ADG96742	Single ch
21	66	100.0	245	7 ADG98057	TNF proli
22	66	100.0	245	8 ADE83862	Chemokine
23	66	100.0	245	8 ADG34308	Neurokini
24	66	100.0	245	8 ADG34313	Neurokini
25	66	100.0	246	5 ABP45902	Human Bly

26	66	100.0	246	5 ABP45906	Human Bly
27	66	100.0	246	7 ADG96733	Single ch
28	66	100.0	246	7 ADG96729	Single ch
29	66	100.0	246	8 ADE83872	Chemokine
30	66	100.0	247	5 ABP45671	Human Bly
31	66	100.0	247	5 ABP45432	Human Bly
32	66	100.0	247	5 ABP45923	Human Bly
33	66	100.0	247	5 ABP45917	Human Bly
34	66	100.0	247	5 ABP45696	Human Bly
35	66	100.0	247	5 ABP45888	Human Bly
36	66	100.0	247	7 ADG30413	Human GMB
37	66	100.0	247	7 ADG30455	Human GMB
38	66	100.0	247	7 ADG96715	Single ch
39	66	100.0	247	7 ADG96498	Single ch
40	66	100.0	247	7 ADG96744	Single ch
41	66	100.0	247	7 ADG96259	Single ch
42	66	100.0	247	7 ADG96750	Single ch
43	66	100.0	247	7 ADG96523	Single ch
44	66	100.0	247	8 ADE83874	Chemokine
45	66	100.0	247	8 ADG34304	Neurokini

ALIGNMENTS

RESULT 1
AAY79071
ID AAY79071 standard; peptide; 13 AA.
XX
AC AAY79071;
XX
DT 12-JUN-2000 (first entry)
XX
DE Anti-factor IX/IXa antibody L chain V domain CDR1 amino acid sequence.
XX
KW Complementarity determining region 1; CDR1; antibody; Gla domain;
KW factor IX/IXa; blood coagulation; deep venous thrombosis; light chain;
KW arterial thrombosis; unstable angina; post myocardial infarction;
KW coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;
KW percutaneous transluminal coronary angioplasty; PTCA; inflammation;
KW septic shock; hypotension; adult respiratory distress syndrome; ARDS;
KW arterial fibrillation; disseminated intravascular coagulopathy; DIC.
XX
OS Homo sapiens.
XX
FN WC200012562-A1.
XX
PD 09-MAR-2000.
XX
PF 26-AUG-1999; 99WO-US019453.
XX
PR 28-AUG-1998; 98US-0098233P.
PR 03-MAR-1999; 99US-0122767P.
XX
(GETH) GENENTECH INC.
XX
PI Adams CW, Devaux B, Eaton DL, Hass PE, Judice JK, Kirchhofer D;
Suggett S;
XX
DR WPI; 2000-256595/22.
XX
XX Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-carboxyglutamic acid domains useful as anti-coagulant in thrombosis, stroke, and post myocardial infarction.
XX
PS Claim 8; Fig 2; 84pp; English.
XX
CC This sequence represents a complementarity determining region 1 (CDR1) of the light chain variable domain of a human anti-factor IX/IXa Gla domain antibody. Factor IXa is a vitamin K dependent plasma serine protease that participates in the blood coagulation pathways. The Gla domain of factor IXa and its zymogen factor IX contains important structural determinants for interaction with high affinity binding sites on vascular endothelial

CC cells and platelets. Compositions comprising the antibodies are used for
 CC the treatment or prophylaxis of thrombotic or coagulopathic diseases or
 CC disorders in a mammal for which inhibiting a FIX/IXa mediated event is
 CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
 CC angina, post myocardial infarction, post surgical thrombosis, coronary
 CC artery bypass graft (CABG), percutaneous transluminal coronary
 CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
 CC inflammation, septic shock, hypotension, adult respiratory distress
 CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
 CC coagulopathy (DIC)
 XX
 SQ Sequence 13 AA;

Query Match 100.0%; Score 66; DB 3; Length 13;
 Best Local Similarity 100.0%; Pred. No. 0.00029; Mismatches 0; Gaps 0;
 Matches 13; Conservative 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
 |||||
 Db 1 SGSTSNIGNNYVS 13

RESULT 2

AAU02544
 ID AAU02544 standard; protein; 109 AA.

XX AAU02544;

DT 29-AUG-2001 (first entry)

DE Anti-adipocyte monoclonal antibody light chain, FAT 31.

KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;

KW heart disease; complementarity determining region; CDR.

XX Homo sapiens.

XX WO200127279-A1.

XX 19-APR-2001.

XX 11-OCT-2000; 2000WO-GB003900.

XX 12-OCT-1999; 99US-0158812P.

XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Edwards BM, Main SH, Vaughan TJ;

XX WPI; 2001-282031/29.

DR N-PSDB; AAS03444.

XX Panel of specific binding members of antibody molecules which bind to
 PT whole adipocytes is used in the treatment of obesity and obesity related
 PT diseases.

PS Claim 1; Page 120; 182pp; English.

XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies

CC for different types of fat deposits can also be produced e.g. intra-
 CC abdominal fat associated with heart disease
 XX
 SQ Sequence 109 AA;

Query Match 100.0%; Score 66; DB 4; Length 109;
 Best Local Similarity 100.0%; Pred. No. 0.0026;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
 |||||
 Db 23 SGSTSNIGNNYVS 35

RESULT 3

AAU02558
 ID AAU02558 standard; protein; 110 AA.

XX AAU02558;

XX 29-AUG-2001 (first entry)

XX Anti-adipocyte monoclonal antibody light chain, FAT 44.

KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;

KW heart disease; complementarity determining region; CDR.

XX Homo sapiens.

XX WO200127279-A1.

XX 19-APR-2001.

XX 11-OCT-2000; 2000WO-GB003900.

XX 12-OCT-1999; 99US-0158812P.

XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Edwards BM, Main SH, Vaughan TJ;

XX WPI; 2001-282031/29.

DR N-PSDB; AAS03458.

XX Panel of specific binding members of antibody molecules which bind to
 PT whole adipocytes is used in the treatment of obesity and obesity related
 PT diseases.

PS Claim 1; Page 128-129; 182pp; English.

XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC abdominal fat associated with heart disease

XX Sequence 110 AA;

Query Match 100.0%; Score 66; DB 4; Length 110;
 Best Local Similarity 100.0%; Pred. No. 0.0026;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
 |||||
 Db 23 SGSTSNIGNNYVS 35

RESULT 4

AAU02612
 ID AAU02612 standard; protein; 110 AA.

AC AAU02612;

XX 29-AUG-2001 (first entry)

XX Anti-adipocyte monoclonal antibody light chain, FAT 99.

XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KW heart disease; complementarity determining region; CDR.

XX Homo sapiens.

XX WO200127279-A1.

XX 19-APR-2001.

XX 11-OCT-2000; 2000WO-GB003900.

XX 12-OCT-1999; 99US-0158812P.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Edwards BM, Main SH, Vaughan TJ;

XX WPI; 2001-282031/29.

XX N-PSDB; AAS03512.

XX Panel of specific binding members of antibody molecules which bind to
 PT whole adipocytes is used in the treatment of obesity and obesity related
 PT diseases.

XX Claim 1; Page 163; 182pp; English.

XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-
 CC abdominal fat associated with heart disease

XX Sequence 110 AA;

Query Match 100.0%; Score 66; DB 4; Length 110;
 Best Local Similarity 100.0%; Pred. No. 0.0026;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
 |||||
 Db 23 SGSTSNIGNNYVS 35

RESULT 5

AAU02627

ID AAU02627 standard; protein; 110 AA.

XX AAU02627;

XX 29-AUG-2001 (first entry)

XX Anti-adipocyte monoclonal antibody light chain, FAT 112.

XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KW heart disease; complementarity determining region; CDR.

XX Homo sapiens.

XX WO200127279-A1.

XX 19-APR-2001.

XX 11-OCT-2000; 2000WO-GB003900.

XX 12-OCT-1999; 99US-0158812P.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Edwards BM, Main SH, Vaughan TJ;

XX WPI; 2001-282031/29.

XX N-PSDB; AAS03527.

XX Panel of specific binding members of antibody molecules which bind to
 PT whole adipocytes is used in the treatment of obesity and obesity related
 PT diseases.

XX Claim 1; Page 172; 182pp; English.

XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-
 CC abdominal fat associated with heart disease

XX Sequence 110 AA;

Query Match 100.0%; Score 66; DB 4; Length 110;
 Best Local Similarity 100.0%; Pred. No. 0.0026;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
 |||||
 Db 23 SGSTSNIGNNYVS 35

RESULT 6

AAU02629

ID AAU02629 standard; protein; 110 AA.

XX AAU02629;

XX 29-AUG-2001 (first entry)

XX Anti-adipocyte monoclonal antibody light chain, FAT 113.

XX

KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KW heart disease; complementarity determining region; CDR.
 XX Homo sapiens.
 XX WO200127279-A1.
 XX 19-APR-2001.
 XX 11-OCT-2000; 2000WO-GB003900.
 XX 12-OCT-1999; 99US-0158812P.
 XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX Edwards BM, Main SH, Vaughan TJ;
 XX WPI; 2001-282031/29.
 XX N-PSDB; AAS03529.
 XX Panel of specific binding members of antibody molecules which bind to
 XX whole adipocytes is used in the treatment of obesity and obesity related
 XX diseases.
 XX Claim 1; Page 173; 182pp; English.
 XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 XX sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 XX and heavy chain complementarity determining regions (CDR) of the
 XX invention. The antibodies can be used in the treatment of obesity and
 XX obesity related diseases. The antibodies can be used to deliver drugs or
 XX pro-drugs directly to the fat mass of an obese patient or the antibody
 XX can be used as a therapeutic itself. Antibodies binding specifically to
 XX adipocytes can be used to activate the immune system to destroy the cells
 XX by complement mediated lysis. The antibodies may be labeled with a
 XX detectable label such as radiolabel, fluorescent or chemical group and
 XX used in methods of diagnosis in human subjects e.g. to determine the
 XX presence of adipocyte antigen on the surface of an adipocyte to detect or
 XX determine the presence or level of adipocytes in a cell or tissue sample.
 XX The antibodies can be used as an alternative means of treatment for obese
 XX patients other than undergoing surgery to remove excess fat. Antibodies
 XX for different types of fat deposits can also be produced e.g. intra-
 XX abdominal fat associated with heart disease
 XX Sequence 110 AA;
 SQ
 Query Match 100.0%; Score 66; DB 4; Length 110;
 Best Local Similarity 100.0%; Pred. No. 0.0026;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGSTSNIGNNYVS 13
 DB 23 SGSTSNIGNNYVS 35
 RESULT 7
 AAU02542
 ID AAU02542 standard; protein; 111 AA.
 XX AAU02542;
 XX 29-AUG-2001 (first entry)
 XX Anti-adipocyte monoclonal antibody light chain, FAT 30.
 XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 XX heart disease; complementarity determining region; CDR.
 XX Homo sapiens.
 XX WO200127279-A1.
 XX 19-APR-2001.

XX 11-OCT-2000; 2000WO-GB003900.
 XX 12-OCT-1999; 99US-0158812P.
 XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX Edwards BM, Main SH, Vaughan TJ;
 XX WPI; 2001-282031/29.
 XX N-PSDB; AAS03442.
 XX Panel of specific binding members of antibody molecules which bind to
 XX whole adipocytes is used in the treatment of obesity and obesity related
 XX diseases.
 XX Claim 1; Page 118-119; 182pp; English.
 XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 XX sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 XX and heavy chain complementarity determining regions (CDR) of the
 XX invention. The antibodies can be used in the treatment of obesity and
 XX obesity related diseases. The antibodies can be used to deliver drugs or
 XX pro-drugs directly to the fat mass of an obese patient or the antibody
 XX can be used as a therapeutic itself. Antibodies binding specifically to
 XX adipocytes can be used to activate the immune system to destroy the cells
 XX by complement mediated lysis. The antibodies may be labeled with a
 XX detectable label such as radiolabel, fluorescent or chemical group and
 XX used in methods of diagnosis in human subjects e.g. to determine the
 XX presence of adipocyte antigen on the surface of an adipocyte to detect or
 XX determine the presence or level of adipocytes in a cell or tissue sample.
 XX The antibodies can be used as an alternative means of treatment for obese
 XX patients other than undergoing surgery to remove excess fat. Antibodies
 XX for different types of fat deposits can also be produced e.g. intra-
 XX abdominal fat associated with heart disease
 XX Sequence 111 AA;
 SQ
 Query Match 100.0%; Score 66; DB 4; Length 111;
 Best Local Similarity 100.0%; Pred. No. 0.0027;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGSTSNIGNNYVS 13
 DB 23 SGSTSNIGNNYVS 35
 RESULT 8
 AAU02551
 ID AAU02551 standard; protein; 111 AA.
 XX AAU02551;
 XX 29-AUG-2001 (first entry)
 XX Anti-adipocyte monoclonal antibody light chain, FAT 37.
 XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 XX heart disease; complementarity determining region; CDR.
 XX Homo sapiens.
 XX WO200127279-A1.
 XX 19-APR-2001.
 XX 11-OCT-2000; 2000WO-GB003900.
 XX 12-OCT-1999; 99US-0158812P.
 XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX Edwards BM, Main SH, Vaughan TJ;
 XX PI

XX DR WPI; 2001-282031/29.
 XX DR N-PSDB; AAS03451.
 XX PT Panel of specific binding members of antibody molecules which bind to
 XX PT whole adipocytes is used in the treatment of obesity and obesity related
 XX PT diseases.
 XX PS Claim 1; Page 124; 182pp; English.
 XX CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 XX CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 XX CC and heavy chain complementarity determining regions (CDR) of the
 XX CC invention. The antibodies can be used in the treatment of obesity and
 XX CC obesity related diseases. The antibodies can be used to deliver drugs or
 XX CC pro-drugs directly to the fat mass of an obese patient or the antibody
 XX CC can be used as a therapeutic itself. Antibodies binding specifically to
 XX CC adipocytes can be used to activate the immune system to destroy the cells
 XX CC by complement mediated lysis. The antibodies may be labeled with a
 XX CC detectable label such as radiolabel, fluorescent or chemical group and
 XX CC used in methods of diagnosis in human subjects e.g. to determine the
 XX CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 XX CC determine the presence or level of adipocytes in a cell or tissue sample.
 XX CC The antibodies can be used as an alternative means of treatment for obese
 XX CC patients other than undergoing surgery to remove excess fat. Antibodies
 XX CC for different types of fat deposits can also be produced e.g. intra-
 XX CC abdominal fat associated with heart disease
 XX SQ Sequence 111 AA;
 Query Match 100.0%; Score 66; DB 4; Length 111;
 Best Local Similarity 100.0%; Pred. No. 0.0027;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGSTSNIGNNYVS 13
 |||||
 Db 24 SGSTSNIGNNYVS 36
 RESULT 9
 ABP45887
 ID ABP45887 standard; protein; 240 AA.
 XX AC ABP45887;
 XX DT 19-AUG-2002 (first entry)
 XX DE Human Blys binding scFv SEQ ID 1898.
 KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX OS Homo sapiens.
 XX FN WO200202641-A1.
 XX PD 10-JAN-2002.
 XX PF 15-JUN-2001; 2001WO-US019110.
 XX PR 16-JUN-2000; 2000US-0212210P.
 XX PR 17-OCT-2000; 2000US-0240816P.
 XX PR 16-MAR-2001; 2001US-0276248P.
 XX PR 21-MAR-2001; 2001US-0277379P.
 XX PR 25-MAY-2001; 2001US-0293499P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX PT

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX WPI; 2002-114799/15.
 XX PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
 XX PT diagnosis and treatment of cancers and immune disorders.
 XX PS Claim 1; Page 2666-2667; 3148pp; English.
 XX CC This invention describes novel antibodies that immunospecifically bind to
 XX CC B Lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 XX CC tumour necrosis factor (TNF) super family and induces B cell
 XX CC proliferation and differentiation. The antibodies of the invention have
 XX CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 XX CC antirheumatic and antiAIDS activity and can be used in vaccines to
 XX CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 XX CC and so may be used to detect and quantitate the presence of Blys in
 XX CC biological samples and may be used in this way to diagnose disease
 XX CC associated with aberrant expression of Blys. They may also be
 XX CC administered to treat diseases associated with aberrant Blys expression
 XX CC and activity such as cancer, immune, and autoimmune disorders and
 XX CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 XX CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 XX CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 XX CC the antibodies and fragments of the antibodies described in the method of
 XX CC the invention
 XX SQ Sequence 240 AA;
 Query Match 100.0%; Score 66; DB 5; Length 240;
 Best Local Similarity 100.0%; Pred. No. 0.0059;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SGSTSNIGNNYVS 13
 |||||
 Db 153 SGSTSNIGNNYVS 165
 RESULT 10
 ADG96714
 ID ADG96714 standard; protein; 240 AA.
 XX AC ADG96714;
 XX DT 11-MAR-2004 (first entry)
 XX DE Single chain antibody that immunospecifically binds Blys SeqID 1898.
 KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
 KW B cell proliferation; differentiation; scFv; myasthenia gravis;
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
 KW carcinoma; lymphoma; antirheumatic; antiallergic; neuroprotective;
 KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.
 XX OS Unidentified.
 XX FN WO2003055979-A2.
 XX PD 10-JUL-2003.
 XX PF 14-NOV-2002; 2002WO-US036496.
 XX PR 16-NOV-2001; 2001US-0331469P.
 XX PR 19-DEC-2001; 2001US-0340817P.
 XX (HUMA-) HUMAN GENOME SCI INC.
 XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX WPI; 2003-505530/47.
 XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator
 XX (Blys), useful for detecting and treating diseases or disorders e.g.

rheumatoid arthritis, asthma and leukemia.
Example 1; SEQ ID NO 1898; 394pp; English.

This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BlyS). The BlyS gene has been mapped to chromosome 13q34 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFvs) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BlyS. The present invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BlyS or its receptor. As such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various activities such as antitumouric, antiarthritic, neuroprotective, antiinflammatory, antiaesthetic, antiatherogenic and cytostatic. This polypeptide sequence is a single chain antibody that binds BlyS of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 240 AA;

Query Match 100.0%; Score 66; DB 7; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.0059;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
| | | | |
DB 153 SGSTSNIGNNYVS 165

RESULT 11
ADG34301

ID ADG34301 standard; protein; 242 AA.
AC
ADG34301;
XX
XX
DT 26-FEB-2004 (first entry)
DE Neurokinin B antibody SEQ ID NO:24.
XX
XX
KW antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
hypertension; pre-eclampsia; NKB.
XX
OS Synthetic.
XX
PN WO2003102136-A2.
XX
PD 11-DEC-2003.
XX
PF 29-MAY-2003; 2003WO-US016802.
PR 30-MAY-2002; 2002US-0383802P.
PS (HUMA-) HUMAN GENOME SCI INC.
PT New antibody that specifically binds neurokinin B, useful for preparing a composition for treating or preventing hypertension or preeclampsia.
XX
OS Synthetic.
XX
PN WO2003102136-A2.
XX
PD 11-DEC-2003.
XX
PF 29-MAY-2003; 2003WO-US016802.
PR 30-MAY-2002; 2002US-0383802P.
PS (HUMA-) HUMAN GENOME SCI INC.
PT Rosen CA, Ruben SM;
WPI; 2004-053456/05.
N-PSDB; ADG34282.
XX
XX
PT New antibody that specifically binds neurokinin B, useful for preparing a composition for treating or preventing hypertension or preeclampsia.
XX
XX
Claim 2; SEQ ID NO 24; 127pp; English.

rheumatoid arthritis, asthma and leukemia.
Example 1; SEQ ID NO 1898; 394pp; English.

This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BlyS). The BlyS gene has been mapped to chromosome 13q34 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFvs) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BlyS. The present invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BlyS or its receptor. As such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and lymphoma. Accordingly, they can be described as exhibiting various activities such as antitumouric, antiarthritic, neuroprotective, antiinflammatory, antiaesthetic, antiatherogenic and cytostatic. This polypeptide sequence is a single chain antibody that binds BlyS of the invention. NOTE: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX
SQ Sequence 240 AA;

Query Match 100.0%; Score 66; DB 7; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.0059;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
| | | | |
DB 153 SGSTSNIGNNYVS 165

RESULT 11
ADG34301

ID ADG34301 standard; protein; 242 AA.
AC
ADG34301;
XX
XX
DT 26-FEB-2004 (first entry)
DE Neurokinin B antibody SEQ ID NO:24.
XX
XX
KW antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
hypertension; pre-eclampsia; NKB.
XX
OS Synthetic.
XX
PN WO2003102136-A2.
XX
PD 11-DEC-2003.
XX
PF 29-MAY-2003; 2003WO-US016802.
PR 30-MAY-2002; 2002US-0383802P.
PS (HUMA-) HUMAN GENOME SCI INC.
PT Rosen CA, Ruben SM;
WPI; 2004-053456/05.
N-PSDB; ADG34282.
XX
XX
PT New antibody that specifically binds neurokinin B, useful for preparing a composition for treating or preventing hypertension or preeclampsia.
XX
XX
Claim 2; SEQ ID NO 24; 127pp; English.

The invention relates to a novel antibody specifically binding neurokinin B. An antibody of the invention has hypotensive, and gynaecological activity, and may have a use in gene therapy. The antibody is useful for preparing a composition for treating or preventing hypertension or pre-eclampsia. The present sequence is used in the exemplification of the invention.

XX
SQ Sequence 242 AA;

Query Match 100.0%; Score 66; DB 8; Length 242;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
| | | | |
DB 154 SGSTSNIGNNYVS 166

RESULT 12
ADG34317

ID ADG34317 standard; protein; 242 AA.
XX
ADG34317;
AC
XX
DT 26-FEB-2004 (first entry)
DE Neurokinin B antibody SEQ ID NO:40.
XX
XX
KW antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
hypertension; pre-eclampsia; NKB.
XX
OS Synthetic.
XX
PN WO2003102136-A2.
XX
PD 11-DEC-2003.
XX
PF 29-MAY-2003; 2003WO-US016802.
PR 30-MAY-2002; 2002US-0383802P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
PI Rosen CA, Ruben SM;
WPI; 2004-053456/05.
N-PSDB; ADG34298.
XX
XX
PT New antibody that specifically binds neurokinin B, useful for preparing a composition for treating or preventing hypertension or preeclampsia.
XX
PS Claim 2; SEQ ID NO 40; 127pp; English.
XX
CC The invention relates to a novel antibody specifically binding neurokinin B. An antibody of the invention has hypotensive, and gynaecological activity, and may have a use in gene therapy. The antibody is useful for preparing a composition for treating or preventing hypertension or pre-eclampsia. The present sequence is used in the exemplification of the invention.

XX
SQ Sequence 242 AA;

Query Match 100.0%; Score 66; DB 8; Length 242;
Best Local Similarity 100.0%; Pred. No. 0.006;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
| | | | |
DB 154 SGSTSNIGNNYVS 166

RESULT 13
ABP45916

```

ID ABP45916 standard; protein; 243 AA.
XX AC
XX ABP45916;
XX DT
XX 19-AUG-2002 (first entry)
XX DE
XX Human BlyS binding scFv SEQ ID 1927.
XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.
XX OS
XX Homo sapiens.
XX WO200202641-A1.
XX PN
XX 10-JAN-2002.
XX PD
XX 15-JUN-2001; 2001WO-US019110.
XX PF
XX 16-JUN-2000; 2000US-0212210P.
XX PR
XX 17-OCT-2000; 2000US-0240816P.
XX PR
XX 16-MAR-2001; 2001US-0276248P.
XX PR
XX 21-MAR-2001; 2001US-0277379P.
XX PR
XX 25-MAY-2001; 2001US-0293499P.
XX PA
XX (HUMA-) HUMAN GENOME SCI INC.
XX PA
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PI
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX DR
XX Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
XX diagnosis and treatment of cancers and immune disorders.
XX PS
XX Claim 1; Page 2700-2701; 3148pp; English.
XX CC
XX This invention describes novel antibodies that immunospecifically bind to
XX B Lymphocyte Stimulator (BlyS) polypeptides. BlyS is a member of the
XX tumour necrosis factor (TNF) super family and induces B cell
XX proliferation and differentiation. The antibodies of the invention have
XX cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
XX antirheumatic and antiAIDS activity and can be used in vaccines to
XX inhibit the expression and activity of BlyS. The antibodies bind to BlyS
XX and so may be used to detect and quantitate the presence of BlyS in
XX biological samples and may be used in this way to diagnose disease
XX associated with aberrant expression of BlyS. They may also be
XX administered to treat diseases associated with aberrant BlyS expression
XX and activity such as cancer, immune, and autoimmune disorders and
XX diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
XX immunodeficiency (e.g. common variable immunodeficiency (CVID) and
XX acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
XX the antibodies and fragments of the antibodies described in the method of
XX the invention
XX SQ Sequence 243 AA;
XX Query Match 100.0%; Score 66; DB 5; Length 243;
XX Best Local Similarity 100.0%; Pred. No. 0.006;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SGSTSNIGNNYVS 13
Db 155 SGSTSNIGNNYVS 167
RESULT 14
AAO31147
ID AAO31147 standard; protein; 243 AA.
XX AC
XX AAO31147;
XX DT
XX 06-OCT-2003 (first entry)
XX DE
XX Human CM085C11 scFv protein that specifically binds TR7.
XX Human; protein coordinate data; heavy chain variable domain; VH; cancer;
XX complementarity determining region; CDR; light chain variable domain; VL;
XX TRAIL receptor 7; TR7; tumour necrosis factor; KILLER; death receptor 5;
XX DR5; TRAIL receptor 2; TRAIL-R2; TNF-related apoptosis-inducing ligand;
XX Kaposi's sarcoma; central nervous system; medulloblastoma; neuroblastoma;
XX glioblastoma; graft versus host disease; antibody therapy; neurotropic;
XX AIDS; acquired immune deficiency syndrome; neurodegenerative disorder;
XX immunosuppressive; neuroprotective; antibody therapy; antibody.
XX OS
XX Homo sapiens.
XX WO2003054216-A2.
XX PN
XX 03-JUL-2003.
XX PD
XX 19-DEC-2002; 2002WO-US040597.
XX PF
XX 20-DEC-2001; 2001US-0341237P.
XX PR
XX 05-APR-2002; 2002US-0369877P.
XX PR
XX 04-JUN-2002; 2002US-0384828P.
XX PR
XX 18-JUL-2002; 2002US-0396591P.
XX PR
XX 15-AUG-2002; 2002US-0403370P.
XX PR
XX 13-NOV-2002; 2002US-0425377P.
XX PA
XX (HUMA-) HUMAN GENOME SCI INC.
XX PI
XX Salcedo T, Albert VR, Rosen CA, Humphreys R, Vaughan TJ;
XX WPI; 2003-569250/53.
XX DR
XX N-PSDB; AAL62844.
XX PT
XX New antibody or its fragment, useful for treating, preventing or
XX ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or
XX gastrointestinal cancer, or Kaposi's sarcoma or, graft versus host
XX disease, AIDS.
XX PS
XX Claim 2; Page 288; 301pp; English.
XX CC
XX The invention relates to an isolated antibody or its fragments such as
XX VHCDR1 (heavy chain variable domain complementarity determining region),
XX VHCDR2, VHCDR3, VLCDR1 (light chain variable domain complementarity
XX determining region), VLCDR2 or VLCDR3. The antibody or its fragment
XX immunospecifically binds TRAIL (tumour necrosis factor; TNF-related
XX apoptosis-inducing ligand) receptor 7 (TR7). TR7 is also referred to as
XX TRAIL receptor 2 (TRAIL-R2), death receptor 5 (DR5) and KILLER. The
XX antibody or its fragment is useful for treating, preventing or
XX ameliorating a cancer, e.g. colon, breast, uterine, pancreatic, lung or
XX gastrointestinal cancer or Kaposi's sarcoma or cancer of the central
XX nervous system such as medulloblastoma, neuroblastoma or glioblastoma or
XX graft versus host disease, AIDS (acquired immune deficiency syndrome) or
XX a neurodegenerative disorder. The invention is useful in antibody
XX therapy. The present sequence is human scFv protein that specifically
XX binds TR7
XX SQ Sequence 243 AA;
XX Query Match 100.0%; Score 66; DB 6; Length 243;
XX Best Local Similarity 100.0%; Pred. No. 0.006;
XX Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 SGSTSNIGNNYVS 13
Db 155 SGSTSNIGNNYVS 167
RESULT 15
AAO31147
ID AAO31147 standard; protein; 243 AA.

```

Job time : 100.938 secs

ADG96743
ID ADG96743 standard; protein; 243 AA.
XX
AC ADG96743;
XX
DT 11-MAR-2004 (first entry)
XX
DE Single chain antibody that immunospecifically binds Blys SeqID 1927.
XX
KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
KW B cell proliferation; differentiation; scFv; myasthenia gravis;
KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
KW antiinflammatory; antiasthmatic; antiallergic; cytostatic.
XX
OS Unidentified.
XX
FN WO2003055979-A2.
XX
PD 10-JUL-2003.
XX
PF 14-NOV-2002; 2002WO-US036496.
XX
PR 16-NOV-2001; 2001US-0331469P.
PR 19-DEC-2001; 2001US-0340817P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX
DR WPI; 2003-505530/47.
XX
PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
PT (Blys), useful for detecting and treating diseases or disorders e.g.
PT rheumatoid arthritis, asthma and leukemia.
XX
PS Example 1; SEQ ID NO 1927; 394pp; English.
XX
CC This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antirheumatic, antiallergic, neuroprotective,
CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
CC polypeptide sequence is a single chain antibody that binds Blys of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 243 AA;

Query Match 100.0%; Score 66; DB 7; Length 243;
Best Local Similarity 100.0%; Pred. NO. 0.006;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGTSTNIGNNVYS 13
Db 155 SGTSTNIGNNVYS 167
|||||

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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:02:59 ; Search time 18.0781 Seconds
(without alignments)
69.190 Million cell updates/sec

Title: US-10-614-959-13
Perfect score: 66
Sequence: 1 SGSTSNIGNNYVS 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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Maximum Match 100%
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Database : PIR 79.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	62	93.9	98	2 S36050	Ig lambda chain -
2	62	93.9	111	2 S47009	Ig lambda chain V1
3	62	93.9	111	2 S19664	Ig lambda chain V
4	62	93.9	113	2 A29700	Ig lambda chain V
5	62	93.9	232	2 S25742	Ig lambda chain -
6	62	93.9	235	2 S05270	Ig lambda chain pr
7	59	89.4	130	2 S09712	Ig lambda chain V
8	57	86.4	130	1 L1HUBL	Ig lambda chain pr
9	56	84.8	111	2 S47185	Ig lambda chain pr
10	56	84.8	131	2 S24321	Ig lambda chain pr
11	55	83.3	111	1 L1HUNW	Ig lambda chain V-
12	53	80.3	98	2 S36048	Ig lambda chain -
13	53	80.3	111	1 L1HUNG	Ig lambda chain V-
14	53	80.3	129	2 S78058	Ig lambda chain pr
15	53	80.3	130	2 S78057	Ig lambda chain pr
16	52	78.8	109	1 L1H05P	Ig lambda chain V-
17	50	75.8	98	2 S36046	Ig lambda chain -
18	49	74.2	234	2 S25757	Ig lambda chain -
19	48	72.7	112	2 C44151	Ig lambda chain V
20	46	69.7	216	2 A42193	Ig lambda chain (B
21	45	68.2	98	2 S36047	Ig lambda chain -
22	45	68.2	110	2 S36258	Ig lambda chain V
23	45	68.2	112	2 D44151	Ig lambda chain V
24	45	68.2	117	2 S23627	Ig lambda chain pr
25	45	68.2	233	2 S25752	Ig lambda chain -
26	44	66.7	112	2 A44151	Ig lambda chain V
27	44	66.7	112	2 B44151	Ig lambda chain V
28	44	66.7	235	2 S25754	Ig lambda chain -
29	43.5	65.9	235	2 S14675	Ig lambda chain -

Ig lambda chain pr
Ig lambda chain V
gag, pol and env p
hypothetical prote
Ig light chain V-J
Ig lambda chain V-
Ig lambda chain -
uncharacterized co
Ig lambda chain V
Ig lambda chain V
Ig lambda chain V-
Ig lambda chain V-
S-aminolevulinat
Ig lambda chain V-
Ig lambda chain V-
Ig lambda chain NI

ALIGNMENTS

RESULT 1

S36050

Ig lambda chain - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000

C;Accession: S36050

R;Williams, S.C.

submitted to the EMBL Data Library, April 1993

A;Reference number: S36046

A;Accession: S36050

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-98 <WIL>

A;Cross-references: EMBL:Z22191; NID:g312298; PIDN:CAA80201.1; PID:g312299

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F;15-91/Domain: immunoglobulin homology <IMM>

Query Match 93.9%; Score 62; DB 2; Length 98;

Best Local Similarity 92.3%; Pred. No. 0.001;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13

Db 23 SGSSSNIGNNYVS 35

RESULT 2

S47009

Ig lambda chain V1-J3 region - human

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C;Accession: S47009

R;Mahmoudi, M.; Gasyna, E.; Denomme, G.; Edwards, J.; Bell, D.; Cairns, E.

submitted to the EMBL Data Library, July 1994

A;Description: The role of the immunoglobulin heavy chain in human anti-DNA antibody bin

A;Reference number: S47009

A;Accession: S47009

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-111 <MAH>

A;Cross-references: EMBL:Z35495; NID:g517346; PIDN:CAA84629.1; PID:g517347

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotrimer; immunoglobulin

F;15-91/Domain: immunoglobulin homology <IMM>

Query Match 93.9%; Score 62; DB 2; Length 111;

Best Local Similarity 92.3%; Pred. No. 0.0011;

Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13

Db 23 SGSSSNIGNNYVS 35

Db 23 SGSSSNIGNNYVS 35

RESULT 3

S19664

Ig lambda chain V region (clone alpha-phOx15) - human

C:Species: Homo sapiens (man)

C>Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 20-Jun-2000

C:Accession: S19664; S24444

R:Marks, J.D.; Hoogenboom, H.R.; Bonnert, T.P.; McCafferty, J.; Griffiths, A.D.; Winter, J. Mol. Biol. 222, 581-597, 1991

A:Title: BY-passing immunization. Human antibodies from V-gene libraries displayed on phage

A:Reference number: S19663; MUID:92085276; PMID:1748994

A:Accession: S19664

A:Molecule type: mRNA

A:Residues: 1-111 <MAR>

A:Cross-references: EMBL:X61641

R:Jones, P.T.

submitted to the EMBL Data Library, October 1991

A:Reference number: S24442

A:Accession: S24444

A:Molecule type: mRNA

A:Residues: 1-110, 'W' <JON>

A:Cross-references: EMBL:X61641; NID:g35458; PIDN:CAA43822.1; PID:g1335271

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-91/Domain: immunoglobulin homology <IMM>

Query Match 93.9%; Score 62; DB 2; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.0011;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
|||||

Db 23 SGSSSNIGNNYVS 35

RESULT 4

A29700

Ig lambda chain V region (Zim) - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 21-Jan-2000

C:Accession: A29700

R:Eulitz, M.; Breuer, M.; Linke, R.P.

Biol. Chem. Hoppe-Seyler 368, 863-870, 1987

A:Title: Is the formation of AL-type amyloid promoted by structural peculiarities of immunoglobulin V region?

A:Reference number: A29700; MUID:87299022; PMID:3620114

A:Accession: A29700

A:Molecule type: protein

A:Residues: 1-113 <EUL>

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:14-90/Domain: immunoglobulin homology <IMM>

Query Match 93.9%; Score 62; DB 2; Length 113;
Best Local Similarity 92.3%; Pred. No. 0.0012;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
|||||

Db 22 SGSSSNIGNNYVS 34

RESULT 5

S25742

Ig lambda chain - human

C:Species: Homo sapiens (man)

C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C:Accession: S25742

R:Combrato, G.; Klobbeck, H.G.

Eur. J. Immunol. 21, 1513-1522, 1991

A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda chain

A:Reference number: S16439; MUID:91257162; PMID:1904362

A:Accession: S25742

A>Status: preliminary; translation not shown

A:Molecule type: mRNA

A:Residues: 1-232 <COM>

A:Cross-references: EMBL:X57806; NID:g33709; PIDN:CAA40944.1; PID:g33710

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:147-215/Domain: immunoglobulin homology <IMM>

Query Match 93.9%; Score 62; DB 2; Length 232;
Best Local Similarity 92.3%; Pred. No. 0.0025;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
|||||

Db 39 SGSSSNIGNNYVS 51

RESULT 6

S05270

Ig lambda chain precursor - human

C:Species: Homo sapiens (man)

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000

C:Accession: S05270; S04601

R:Kishimoto, T.

submitted to the EMBL Data Library, March 1989

A:Reference number: S05270

A:Accession: S05270

A:Molecule type: mRNA

A:Residues: 1-235 <KIS1>

A:Cross-references: EMBL:X14583; NID:g33394; PIDN:CAA32725.1; PID:g33395

R:Kishimoto, T.; Okajima, H.; Okumoto, T.; Taniguchi, M.

Nucleic Acids Res. 17, 4385, 1989

A:Title: Nucleotide sequences of the cDNAs encoding the V-regions of H- and L-chains of immunoglobulin lambda chain precursor

A:Reference number: S04601; MUID:89296497; PMID:2500644

A:Accession: S04601

A:Molecule type: mRNA

A:Residues: 1-130 <KIS2>

A:Cross-references: EMBL:X14583

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-235/Product: Ig lambda chain #status predicted <MAT>

F:150-218/Domain: immunoglobulin homology <IMM>

Query Match 93.9%; Score 62; DB 2; Length 235;
Best Local Similarity 92.3%; Pred. No. 0.0025;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
|||||

Db 42 SGSSSNIGNNYVS 54

RESULT 7

S09712

Ig lambda chain V region - human

C:Species: Homo sapiens (man)

C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C:Accession: S09712

R:Hughes-Jones, N.C.; Bye, J.M.; Beale, D.; Coadwell, J.

Biochem. J. 268, 135-140, 1990

A:Title: Nucleotide sequences and three-dimensional modelling of the VH and VL domains of immunoglobulin lambda chain V region

A:Reference number: S09710; MUID:90262535; PMID:2111699

A:Accession: S09712

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-130 <HUG>

A:Cross-references: EMBL:X52109; NID:g31454; PIDN:CAA36343.1; PID:g31455

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:34-110/Domain: immunoglobulin homology <IMM>

```

Query Match      89.4%; Score 59; DB 2; Length 130;
Best Local Similarity 84.6%; Pred. No. 0.0045;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SGSTSNIGNNYVS 13
      |||:|||||
Db      42 SGTSSNIGNNYVS 54

RESULT 8
LiHUNW
Ig lambda chain precursor V-I region (BL2) - human
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 09-Jul-2004
C:Accession: A01966
R:Tejimoto, Y.; Croce, C.M.
Nucleic Acids Res. 12, 8407-8414, 1984
A:Title: Molecular cloning of a human immunoglobulin lambda chain variable sequence.
A:Reference number: A01966; MUID:85062823; PMID:6095199
A:Accession: A01966
A:Molecule type: mRNA
A:Residues: 1-130 <TSU>
A:Cross-references: UNIPROT:P06316; GB:X01147; NID:g33335; PIDN:CAA25598.1; PID:g758087
C:Genetics:
A:Gene: GDB:IGLV@
A:Cross-references: GDB:119342; OMIM:147240
A:Map position: 22q11.2-22q11.2
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-130/Product: Ig lambda chain V-I region (BL2) #status predicted <MAT>
F:20-115/Region: V segment
F:34-110/Domain: immunoglobulin homology <IMM>
F:116-130/Region: J segment
F:41-108/Disulfide bonds: #status predicted

Query Match      86.4%; Score 57; DB 1; Length 130;
Best Local Similarity 84.6%; Pred. No. 0.01;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SGSTSNIGNNYVS 13
      |||:|||||
Db      42 SGTSSNIGNDYVS 54

RESULT 9
S47185
Ig lambda chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S47185
R:McIntosh, R.S.; Tandon, N.; Metcalfe, R.A.; Weetman, A.P.
Submitted to the EMBL Data Library, June 1994
A:Description: Cloning and analysis of IGM anti-thyroglobulin autoantibodies from patien
A:Reference number: S47181
A:Accession: S47185
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-111 <MCI>
A:Cross-references: EMBL:X79782; NID:g506428; PIDN:CAA56178.1; PID:g506429
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-90/Domain: immunoglobulin homology <IMM>

Query Match      84.8%; Score 56; DB 2; Length 111;
Best Local Similarity 84.6%; Pred. No. 0.013;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 SGSTSNIGNNYVS 13
      |||:|||||
Db      22 SGTSSNIGNNYVS 34

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RESULT 10
S24321
Ig lambda chain precursor - human
C:Species: Homo sapiens (man)
C:Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S24321
R:Aucouturier, P.; Khamlichi, A.A.; Preud'homme, J.L.; Bauwens, M.; Touchard, G.; Cogne,
Biochem. J. 285, 149-152, 1992
A:Title: Complementary DNA sequence of human amyloidogenic immunoglobulin light-chain pr
A:Reference number: S24319; MUID:92344562; PMID:1379039
A:Accession: S24321
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-131 <AUC>
A:Cross-references: EMBL:X64134; NID:g32808; PIDN:CAA45495.1; PID:g32809
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:34-110/Domain: immunoglobulin homology <IMM>

Query Match      84.8%; Score 56; DB 2; Length 131;
Best Local Similarity 84.6%; Pred. No. 0.015;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      1 SGSTSNIGNNYVS 13
      |||:|||||
Db      42 SGTSSNIGNNYVS 54

RESULT 11
LiHUNW
Ig lambda chain V-I region (New) - human
C:Species: Homo sapiens (man)
C:Date: 24-Apr-1984 #sequence_revision 24-Apr-1984 #text_change 09-Jul-2004
C:Accession: A01964
R:Langer, B.; Steinmetz-Kayne, M.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 349, 945-951, 1968
A:Title: The complete amino acid sequence of Bence-Jones protein New (lambda type) . Sub
A:Reference number: A01964; MUID:69060892; PMID:4177823
A:Accession: A01964
A:Molecule type: protein
A:Residues: 1-111 <LAN>
A:Cross-references: UNIPROT:P01701
C:Comment: This is a Bence Jones protein.
C:Genetics:
A:Gene: GDB:IGLV@
A:Cross-references: GDB:119342; OMIM:147240
A:Map position: 22q11.2-22q11.2
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: blocked amino end; heterotetramer
F:15-91/Domain: immunoglobulin homology <IMM>
F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #statu
F:22-89/Disulfide bonds: #status predicted

Query Match      83.3%; Score 55; DB 1; Length 111;
Best Local Similarity 76.9%; Pred. No. 0.019;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 SGSTSNIGNNYVS 13
      |||:|||||
Db      23 SGTSSNIGNNYVS 35

RESULT 12
S36048
Ig lambda chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C:Accession: S36048; S36049
R:Williams, S.C.

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submitted to the EMBL Data Library, April 1993

A:Accession: S36046
A:Reference number: S36048
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <HAW>
A:Cross-references: EMBL:Z22189; NID:g312294; PIDN:CAA80199.1; PID:g312295; EMBL:Z22190
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-91/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 53; DB 2; Length 98;
Best Local Similarity 83.3%; Pred. No. 0.037;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVY 12
|||:||||:|
DB 23 SGSSNIGSNVY 34

RESULT 13

LIHUNG
Ig lambda chain V-I region (Nig-64) - human (tentative sequence)
C:Species: Homo sapiens (man)
C:Date: 03-Aug-1984 #sequence_revision 03-Aug-1984 #text_change 09-Jul-2004
C:Accession: A01965
R:Kametani, F.; Takayasu, T.; Suzuki, S.; Shinoda, T.; Okuyama, T.; Shimizu, A.
J. Biochem. 93, 421-429, 1983
A:Reference number: A91970; MUID:83186114; PMID:6404900
A:Accession: A01965
A:Molecule type: protein
A:Residues: 1-111 <KAW>
A:Cross-references: UNIPROT:P01702
C:Genetics:
A:Gene: GDB:IGLV@
A:Cross-references: GDB:119342; OMIM:147240

A:Map position: 22q11.2-22q11.2
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger disulfide bonds.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: blocked amino end; heterotetramer
F:15-91/Domain: immunoglobulin homology <IMM>
F:1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status
F:22-89/disulfide bonds: #status predicted

Query Match 80.3%; Score 53; DB 1; Length 111;
Best Local Similarity 76.9%; Pred. No. 0.042;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVYS 13
|||:||||:|
DB 23 SGSSNIGDNFVS 35

RESULT 14

S78058
Ig lambda chain precursor V-J region (clone mAb 67VL) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C:Accession: S78058; S23723
R:Harindranath, N.
submitted to the EMBL Data Library, August 1990
A:Reference number: S78051
A:Accession: S78058
A:Molecule type: mRNA
A:Residues: 1-129 <HAR>
A:Cross-references: EMBL:X54446; NID:g37923; PIDN:CAA38313.1; PID:g930121
R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and high-affinity IgG1 and IgG2b antibodies

A:Reference number: S23716; MUID:92031262; PMID:1718404

A:Accession: S23723
A:Molecule type: mRNA
A:Residues: 19-129 <HAW>
A:Cross-references: EMBL:X54446
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-18/Domain: signal sequence (fragment) #status predicted <SIG>
F:19-129/Product: Ig lambda chain (fragment) #status predicted <MAT>
F:33-109/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 53; DB 2; Length 129;
Best Local Similarity 83.3%; Pred. No. 0.049;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVY 12
|||:||||:|
DB 41 SGSSNIGSNVY 52

RESULT 15

S78057
Ig lambda chain precursor V-J region (clone mAb 61VL) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C:Accession: S78057; S23722
R:Harindranath, N.
submitted to the EMBL Data Library, August 1990
A:Reference number: S78051
A:Accession: S78057
A:Molecule type: mRNA
A:Residues: 1-130 <HAR>
A:Cross-references: EMBL:X54438; NID:g37920; PIDN:CAA38307.1; PID:g37921
R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Burastero, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and high-affinity IgG1 and IgG2b antibodies

A:Reference number: S23716; MUID:92031262; PMID:1718404

A:Accession: S23722
A:Molecule type: mRNA
A:Residues: 20-130 <HAW>
A:Cross-references: EMBL:X54438
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-130/Product: Ig lambda chain (fragment) #status predicted <MAT>
F:34-110/Domain: immunoglobulin homology <IMM>

Query Match 80.3%; Score 53; DB 2; Length 130;
Best Local Similarity 83.3%; Pred. No. 0.049;
Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNVY 12
|||:||||:|
DB 42 SGSSNIGSNVY 53

Search completed: October 14, 2005, 16:23:38
Job time : 18.0781 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 15:51:44 ; Search time 86.5312 Seconds
(without alignments)
76.932 Million cell updates/sec

Title: US-10-614-959-13
Perfect score: 66
Sequence: 1 SGSTSNIGNNYVS 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	86.4	130	1 LV1G HUMAN	P06316 homo sapien
2	56	84.8	101	2 Q81ZD8	Q81ZD8 homo sapien
3	55	83.3	110	2 Q8TE63	Q8TE63 homo sapien
4	55	83.3	111	1 LV1C HUMAN	P01701 homo sapien
5	53	80.3	108	2 Q96S80	Q96S80 homo sapien
6	53	80.3	111	1 LV1D HUMAN	P01702 homo sapien
7	52	78.8	109	1 LV1I HUMAN	P06888 homo sapien
8	52	78.8	235	2 Q6IN99	Q6IN99 homo sapien
9	51	77.3	236	2 Q8NEJ1	Q8NEJ1 homo sapien
10	49	74.2	237	2 Q6DHW4	Q6DHW4 homo sapien
11	45	68.2	235	2 Q6GMW6	Q6GMW6 homo sapien
12	44	66.7	221	2 Q87LH3	Q87LH3 vibrio para
13	44	66.7	326	2 Q7SCJ5	Q7SCJ5 neurospora
14	44	66.7	441	2 Q6JRX2	Q6JRX2 phthorimaea
15	43	65.2	1170	2 Q7WZ99	Q7WZ99 pseudomonas
16	43	65.2	1357	2 Q9W4M4	Q9W4M4 drosophila
17	43	65.2	2186	1 Y152_CABEL	P34431 caenorhabdi
18	43	65.2	2272	2 Q17329	Q17329 caenorhabdi
19	43	65.2	2500	2 Q96223	Q96223 plasmodium
20	42	63.6	236	2 Q6GMV7	Q6GMV7 homo sapien
21	42	63.6	348	2 Q97KX3	Q97KX3 clostridium
22	42	63.6	633	1 ACES_ELEEL	Q42275 electrophor
23	41	62.1	111	1 LV6D_HUMAN	P06318 homo sapien
24	41	62.1	112	1 LV1H_HUMAN	P06887 homo sapien
25	41	62.1	388	2 Q9VRW7	Q9VRW7 drosophila
26	41	62.1	414	1 HEM1_RICPR	Q95CB8 rickettsia
27	41	62.1	414	2 Q6RVS3	Q6RVS3 rickettsia
28	41	62.1	847	2 Q8BK59	Q6BK59 debaryomyce
29	41	62.1	958	2 Q7ART8	Q7ART8 plasmodium
30	41	62.1	1272	2 Q95SG4	Q95SG4 drosophila
31	41	62.1	1272	2 Q9W117	Q9W117 drosophila

32	41	62.1	1298	2	Q81IE2	Q81IE2 drosophila
33	41	62.1	1336	2	Q81IA0	Q81IA0 drosophila
34	41	62.1	1701	2	Q81I50	Q81I50 plasmodium
35	40	60.6	109	1	LV1F_HUMAN	P04208 homo sapien
36	40	60.6	112	1	LV1B_HUMAN	P01700 homo sapien
37	40	60.6	159	2	Q8GPE2	Q8GPE2 photorhabdu
38	40	60.6	314	2	Q76611	Q76611 caenorhabdi
39	40	60.6	315	2	Q8WIR8	Q8WIR8 lycopersico
40	40	60.6	410	2	Q8FI25	Q8FI25 escherichia
41	40	60.6	415	2	Q9FJF2	Q9FJF2 arabidopsis
42	40	60.6	514	2	Q47936	Q47936 francisella
43	40	60.6	561	2	Q7R259	Q7R259 neurospora
44	40	60.6	569	2	Q7Q967	Q7Q967 anopheles g
45	40	60.6	715	1	CLPB_MYCPN	P75247 mycoplasma

ALIGNMENTS

RESULT 1
LV1G_HUMAN STANDARD; PRT; 130 AA.
AC P06316;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig lambda chain V-I region BL2 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ON NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85062823; PubMed=6095199;
RA Tsujimoto Y., Croce C.M.;
RT "Molecular cloning of a human immunoglobulin lambda chain variable sequence.";
RL Nucleic Acids Res. 12:8407-8414(1984).

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EMBL; X01147; CAA25598.1; --
PIR; A01966; L1HUBL.
HSSP; P01703; 7FAB.
GO; GO:0005576; C:extracellular; NAS.
GO; GO:0003823; F:antigen binding; NAS.
GO; GO:0006955; P:immune response; NAS.
InterPro; IPR007110; Ig-like.
Pfam; PF00047; Ig; 1.
SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG_LIKE; 1.
Immunoglobulin V region; Signal.
SIGNAL 1 19
FT CHAIN 20 130 Ig lambda chain V-I region BL2.
FT DOMAIN 20 115 V segment.
FT DOMAIN 116 130 J segment.
FT DISULFID 41 108 By similarity.
FT NON_TER 130 130
SQ SEQUENCE 130 AA; 13564 MW; FA44BB17D3A55EBF CRC64;

Query Match 86.4%; Score 57; DB 1; Length 130;
Best Local Similarity 84.6%; Pred. No. 0.069;
Matches 11; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 SGSTSNIGNNYVS 13
||||:|||||:|

Db 42 SGSSNIGNDNYVS 54

RESULT 2

Q81ZD8 PRELIMINARY; PRT; 101 AA.
AC Q81ZD8;
DT 01-WAR-2003 (TReMBLrel. 23, Created)
DT 01-WAR-2003 (TReMBLrel. 23, Last sequence update)
DT 01-WAR-2004 (TReMBLrel. 26, Last annotation update)
DE Anti-thyroglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jang Y.-J., Chung J., Park J.-Y.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY145444; AAN64328.1; -.
DR HSP; P01703; 7FAB.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT NON_TER 101
SQ SEQUENCE 101 AA; 10374 MW; 1506C2D9AACBA793 CRC64;

Query Match 84.8%; Score 56; DB 2; Length 101;

Best Local Similarity 84.6%; Pred. No. 0.079;

Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
Query Match 84.8%; Score 56; DB 2; Length 101;
Best Local Similarity 84.6%; Pred. No. 0.079;
Matches 11; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Q8TE63 PRELIMINARY; PRT; 110 AA.

AC Q8TE63;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Immunoglobulin light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95007525; PubMed=7923137;
RA Hall B.L., Murray J.H., Haspel M.V., Kobrin B.J.;
RT "Establishment, molecular rescue, and expression of 123AV16-1, a tumor-reactive human monoclonal antibody.";
RL Cancer Res 54:5178-5185(1994).
DR EMBL; L33985; AAL68704.1; -.
DR HSP; P01703; 7FAB.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER 1
FT CHAIN <1 >110 immunoglobulin light chain variable region.
FT NON_TER 110
FT NON_TER 110
SQ SEQUENCE 110 AA; 11479 MW; 599D1628F8F5437C CRC64;

Query Match 83.3%; Score 55; DB 2; Length 110;
Best Local Similarity 76.9%; Pred. No. 0.13;
Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13

||:|||||:
Db 23 SGTSSNIGNNFVS 35

RESULT 4

LVIC_HUMAN
ID LVIC_HUMAN STANDARD; PRT; 111 AA.
AC P01701;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-I region NEW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=69060892; PubMed=4177823;
RA Langer B., Steinmetz-Kayne M., Hilschmann N.;
RT "The complete amino acid sequence of Bence Jones protein New (lambda-type). Subgroups in the variable part of immunoglobulin L-chains of the lambda-type.";
RL Hoppe-Seyler's Z. Physiol. Chem. 349:945-951(1968).
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01964; L1HUNW.
DR HSP; P01703; 7FAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region; Pyrolydine carboxylic acid.
FT DOMAIN 1 105 IG-like.
FT MOD_RES 1 1 Pyrolydine carboxylic acid.
FT DISULFID 22 89 By similarity.
FT NON_TER 111
SQ SEQUENCE 111 AA; 11453 MW; AAECBCA3C49F2AD3 CRC64;

Query Match 83.3%; Score 55; DB 1; Length 111;

Best Local Similarity 76.9%; Pred. No. 0.13;

Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13

||:|||||:
Db 23 SGTSSNIGNNFVS 35

RESULT 5

Q96SB0 PRELIMINARY; PRT; 108 AA.
AC Q96SB0;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
DE Anti-streptococcal/anti-myoisin immunoglobulin lambda light chain variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikman A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyreactive monoclonal antibodies from rheumatic carditis: human anti-N-acetylglucosamine/anti-myoisin

RT antibody V region genes.";
 RL J. Immunol. 161:2020-2031(1998).
 DR EMBL; U96394; AAB68783.1; -
 DR PDB; 1KU4; Model; L=1-108.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS0835; IG LIKE; 1.
 FT NON TER 1
 SQ SEQUENCE 108 AA; 11594 MW; F4B5DC478A043F48 CRC64;

Query Match 80.3%; Score 53; DB 2; Length 108;
 Best Local Similarity 83.3%; Pred. No. 0.29;
 Matches 10; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYV 12
 |||:|||||
 Db 23 SGSSNIGSNYV 34

RESULT 6

LVID_HUMAN STANDARD; PRT; 111 AA.
 AC P01702;
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DS Ig lambda chain V-I region NIG-64.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.

RX MEDLINE=83186114; PubMed=6404900;
 RA Kametani F., Takayasu T., Suzuki S., Shinoda T., Okuyama T.,
 RA Shimizu A.;
 RT "Comparative studies on the structure of the light chains of human
 RT immunoglobulins. IV. Assignment of a subgroup.",
 RL J. Biochem. 93:421-429(1983).

CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR PIR; A01965; LIHUNG.
 DR HSSP; P01703; 7FAB.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.

DR PROSITE; PS0835; IG LIKE; 1.

KW Direct protein sequencing; Immunoglobulin V region;
 KW Pyrolydione carboxylic acid. Ig-like.

FT DOMAIN 1 105
 FT MOD RES 1 1
 FT DISULFID 22 89
 FT NON TER 111 111

FT Pyrolydione carboxylic acid.
 FT NON TER 111 111
 SQ SEQUENCE 111 AA; 11454 MW; A21C6121C18A61E0 CRC64;

Query Match 80.3%; Score 53; DB 1; Length 111;
 Best Local Similarity 76.9%; Pred. No. 0.29;
 Matches 10; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
 |||:|||||
 Db 23 SGSSNIGDNFVS 35

RESULT 7

LVID_HUMAN STANDARD; PRT; 109 AA.
 AC P06888;
 DT 01-JAN-1988 (Rel. 06, Created)

DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Ig lambda chain V-I region EPS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=86000126; PubMed=3929803;
 RA Toft K.G., Sletten K., Husby G.;
 RT "The amino-acid sequence of the variable region of a carbohydrate-
 RT containing amyloid fibril protein EPS (immunoglobulin light chain,
 RT type lambda).";
 RL Biol. Chem. Hoppe-Seyler 366:617-625(1985).
 CC -I- MISCELLANEOUS: Residues 1-2, 56-62, and 74-78 and the sequenced
 CC peptides were positioned by homology.
 CC -I- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR PIR; A24656; LIHUEP.

DR HSSP; P01703; 7FAB.

DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; F:antigen binding; NAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS0835; IG LIKE; 1.

KW Amyloid; Direct protein sequencing; Glycoprotein;

KW Immunoglobulin V region.

FT DOMAIN 1 105

FT CARBOHYD 104 104

FT DISULFID 22 89

FT NON TER 109 109

SQ SEQUENCE 109 AA; 11414 MW; 556A313E24D5ACT73 CRC64;

Query Match 78.8%; Score 52; DB 1; Length 109;

Best Local Similarity 83.3%; Pred. No. 0.42;

Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYV 12
 |||:|||||
 Db 23 SGSSNIGKNYV 34

RESULT 8

Q6IN99 PRELIMINARY; PRT; 235 AA.
 AC Q6IN99;

DT 05-JUL-2004 (TRENBLrel. 27, Created)

DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)

DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)

DE IGLC2 protein.

GN Name=IGLC2;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Pancreas;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Colling F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hong L.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Baha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

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RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Pancreas;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC072392; AAH72392.1; -.
DR HSSP; P01842; IAKQ.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGc1; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 235 AA; 24888 MW; 90C95D5E87A6BCC1 CRC64;

Query Match 78.8%; Score 52; DB 2; Length 235;
Best Local Similarity 76.9%; Pred. No. 0.9;
Matches 10; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGRSTNIGNNYVS 13
|| :|||||:|
Db 42 SGRSSNIGNSYVS 54

RESULT 9
Q8NEJ1 PRELIMINARY; PRT; 236 AA.
ID Q8NEJ1
AC Q8NEJ1
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-WAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC075843; AAH75843.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.

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RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030984; AAH30984.1; -.
DR HSSP; P01703; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; C1-set; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 1.
SQ SEQUENCE 236 AA; 25024 MW; 1703B77942630E08 CRC64;

Query Match 77.3%; Score 51; DB 2; Length 236;
Best Local Similarity 83.3%; Pred. No. 1.3;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 SGRSTNIGNNYV 12
||| :|||:|
Db 42 SGRSRNIGNSYV 53

RESULT 10
Q6DHW4 PRELIMINARY; PRT; 237 AA.
ID Q6DHW4
AC Q6DHW4
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RP TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC075843; AAH75843.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.

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DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00407; Ig; 2.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Igc1; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 237 AA; 25108 MW; 6814170F7E784825 CRC64;

Query Match 74.2%; Score 49; DB 2; Length 237;
Best Local Similarity 83.3%; Pred.No. 3;
Matches 10; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGSTSNIIGNYV 12
Db 42 SGSSSNIIGNYV 53

RESULT 11
Q6GMW6 PRELIMINARY; PRT; 235 AA.
AC Q6GMW6;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Bernge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Lequellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Faney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC073784; AA073784.1; -.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF07654; CI-set; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00409; Ig; 2.
DR SMART; SM00407; Igc1; 1.
DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 24803 MW; 058B05F61118F1B8 CRC64;

Query Match 68.2%; Score 45; DB 2; Length 235;
Best Local Similarity 69.2%; Pred.No. 14;
Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 SGSTSNIIGNYVS 13
Db 42 SGSSSNIIGNSVN 54

RESULT 12
Q87LH3 PRELIMINARY; PRT; 221 AA.
AC Q87LH3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative short-chain dehydrogenase.
GN OrderedLocusNames=VP2639;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shinagawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
RT distinct from that of V. cholerae.";
RL Lancet 361:743-749(2003).
DR EMBL; AP005082; BAC6902.1; -.
DR GO; GO:0016491; P:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002198; ADH short.
DR InterPro; IPR002347; Adh_short_C2.
DR Pfam; PF00166; adh_short; 1.
DR PRINTS; PR00081; GDHRDH.
KW Complete proteome.
SQ SEQUENCE 221 AA; 23803 MW; D545E953C9AB3A2F CRC64;

Query Match 66.7%; Score 44; DB 2; Length 221;
Best Local Similarity 66.7%; Pred.No. 20;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GSTSNIIGNYVS 13
Db 203 GALANIGNYVS 214

RESULT 13
Q7SGJ5 PRELIMINARY; PRT; 336 AA.
AC Q7SGJ5;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=NCU00836.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
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RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothé G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysseilis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Kryatofova S., Rasmussen C., Metznerberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nuebaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus *Neurospora crassa*.";
CC Nature 0-0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary.
CC EMBL; AABX01000101; EAA34466.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0004553; F:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR000254; CBD_fungal.
DR InterPro; IPR005103; Glyco_hydro_61.
DR Pfam; PF00734; CBM 1; 1.
DR Pfam; PF03443; Glyco_hydro_61; 1.
DR PROSITE; PS00562; CBD_FUNGAL; 1.
KW Hypothetical protein.
SQ SEQUENCE 326 AA; 33269 MW; 61BC539A292B959F CRC64;

Query Match 66.7%; Score 44; DB 2; Length 326;
Best Local Similarity 61.5%; Pred. No. 30;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYV 13
Db |||||:|:|:|

RESULT 14
Q8JRX2 PRELIMINARY; PRT; 441 AA.
AC Q8JRX2;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Late expression factor 4.
GN Name=PhopGV087;
OS Phthorimaea operculella granulovirus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae; Granulovirus.
OX NCBI_TaxID=192584;
RN [1]
RP SEQUENCE FROM N.A.
RA Croizier L., Taha A., Croizier G., Lopez Ferber M.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF499596; AAM70285.1; -.
DR GO; GO:0030528; P:transcription regulator activity; IEA.
DR GO; GO:0045449; P:regulation of transcription; IEA.
DR InterPro; IPR007790; LEF-4.
DR Pfam; PF05098; LEF-4; 1.
SQ SEQUENCE 441 AA; 51639 MW; DC7B3982232E3550 CRC64;

Query Match 66.7%; Score 44; DB 2; Length 441;
Best Local Similarity 66.7%; Pred. No. 41;
Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYV 12
Db ||:|||||

RESULT 15
Q7WZN9

ID Q7WZN9 PRELIMINARY; PRT; 1170 AA.
AC Q7WZN9;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PiliY1.
GN Name=piliY1;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PA14;
RX PubMed=14983043; DOI=10.1073/pnas.0304622101;
RA He J., Baldini R.L., Deziel E., Saucier M., Zhang Q., Liberati N.T.,
RA Lee D., Urbach J., Goodman H.M., Rahme L.G.;
RT "The broad host range pathogen *Pseudomonas aeruginosa* strain PA14
RT carries two pathogenicity islands harboring plant and animal virulence
RT genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:2530-2535(2004).
DR EMBL; AY273871; AAP81276.1; -.
DR InterPro; IPR008707; Neisseria_PilC.
DR Pfam; PF05567; Neisseria_PilC; 1.
SQ SEQUENCE 1170 AA; 128118 MW; 9F4CDF6D681B62F3 CRC64;

Query Match 65.2%; Score 43; DB 2; Length 1170;
Best Local Similarity 70.0%; Pred. No. 1.6e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 GSTSNIGNNY 11
Db ||||:|

Search completed: October 14, 2005, 16:19:55
Job time : 88.5312 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:00:04 ; Search time 25.5938 Seconds
(without alignments)
37.917 Million cell updates/sec

Title: US-10-614-959-13
Perfect score: 66
Sequence: 1 SGSTSNIGNNYVS 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

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- 2: /cgm2_6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgm2_6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgm2_6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgm2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	66	100.0	13	4	US-09-383-667-13
2	62	93.9	98	2	US-08-665-202-37
3	62	93.9	98	4	US-09-315-574-37
4	62	93.9	111	2	US-08-665-202-36
5	62	93.9	111	2	US-08-665-202-42
6	62	93.9	111	2	US-08-665-202-43
7	62	93.9	111	3	US-08-983-607-35
8	62	93.9	111	4	US-09-315-574-36
9	62	93.9	111	4	US-09-315-574-42
10	62	93.9	111	4	US-09-315-574-43
11	62	93.9	112	2	US-08-665-202-39
12	62	93.9	112	3	US-08-983-607-31
13	62	93.9	112	3	US-09-025-769B-18
14	62	93.9	112	4	US-09-315-574-39
15	62	93.9	112	4	US-09-490-070A-18
16	62	93.9	112	4	US-09-490-153-18
17	62	93.9	112	4	US-09-490-324-18
18	62	93.9	114	3	US-09-240-274-62
19	62	93.9	234	4	US-09-372-425A-4
20	62	93.9	258	2	US-08-665-202-5
21	62	93.9	258	4	US-09-315-574-5
22	62	93.9	262	3	US-09-069-821-4
23	62	93.9	262	4	US-09-956-086-4
24	62	93.9	262	4	US-09-956-087-4
25	62	93.9	282	3	US-09-420-592A-7
26	62	93.9	282	4	US-09-985-442-7
27	62	93.9	282	4	US-09-983-580-7

28	61	92.4	111	2	US-08-652-816A-15	Sequence 15, Appl
29	58	87.9	111	2	US-08-665-202-40	Sequence 40, Appl
30	58	87.9	111	4	US-09-315-574-40	Sequence 40, Appl
31	58	87.9	113	1	US-08-211-202-112	Sequence 112, App
32	57	86.4	109	3	US-09-240-274-55	Sequence 55, Appl
33	57	86.4	109	3	US-09-025-769B-32	Sequence 32, Appl
34	57	86.4	109	3	US-09-025-769B-51	Sequence 51, Appl
35	57	86.4	109	4	US-09-490-070A-32	Sequence 32, Appl
36	57	86.4	109	4	US-09-490-070A-51	Sequence 51, Appl
37	57	86.4	109	4	US-09-490-153-32	Sequence 32, Appl
38	57	86.4	109	4	US-09-490-153-51	Sequence 51, Appl
39	57	86.4	109	4	US-09-490-324-32	Sequence 32, Appl
40	57	86.4	109	4	US-09-490-324-51	Sequence 51, Appl
41	55	83.3	110	1	US-08-199-911-2	Sequence 2, Appl
42	53	80.3	98	1	US-08-211-202-111	Sequence 111, App
43	53	80.3	98	2	US-08-665-202-38	Sequence 38, Appl
44	53	80.3	98	4	US-09-315-574-38	Sequence 38, Appl
45	53	80.3	109	3	US-09-240-274-59	Sequence 59, Appl

ALIGNMENTS

RESULT 1

US-09-383-667-13
; Sequence 13, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Haas, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: PI661R2
; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 13
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-383-667-13

Query Match 100.0%; Score 66; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
Db 1 SGSTSNIGNNYVS 13

RESULT 2

US-08-665-202-37
; Sequence 37, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco

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/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/665,202
/ FILING DATE: 13-JUN-1996
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/000,238
/ FILING DATE: 14-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/000,250
/ FILING DATE: 15-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hunter, Tom
/ REGISTRATION NUMBER: 38,498
/ REFERENCE/DOCKET NUMBER: 02307E-061410
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 98 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-665-202-37

Query Match 93.9%; Score 62; DB 2; Length 98;
Best Local Similarity 92.3%; Pred. No. 0.007;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
Db 23 SGSSNIGNNYVS 35

RESULT 3
US-09-315-574-37
/ Sequence 37, Application US/09315574
/ Patent No. 6512097
/ GENERAL INFORMATION:
/ APPLICANT: Marks, James D.
/ APPLICANT: Schier, Robert
/ TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
/ TITLE OF INVENTION: Tumor Antigens
/ NUMBER OF SEQUENCES: 141
/ CORRESPONDENCE ADDRESSES:
/ ADDRESS: Majestic, Parsons, Siebert & Hsue P.C.
/ STREET: Four Embarcadero Center, Suite 1100
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-4106
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/315,574
/ FILING DATE: 20-MAY-99
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/000,238
/ FILING DATE: 14-JUN-1995
/ PRIOR APPLICATION DATA:
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/ APPLICATION NUMBER: US 60/000,250
/ FILING DATE: 15-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/665,202
/ FILING DATE: 13-JUN-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hunter, Tom
/ REGISTRATION NUMBER: 38,498
/ REFERENCE/DOCKET NUMBER: 02307E-061411
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 37:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 98 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-09-315-574-37

Query Match 93.9%; Score 62; DB 4; Length 98;
Best Local Similarity 92.3%; Pred. No. 0.007;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
Db 23 SGSSNIGNNYVS 35

RESULT 4
US-08-665-202-36
/ Sequence 36, Application US/08665202
/ Patent No. 5977322
/ GENERAL INFORMATION:
/ APPLICANT: Marks, James D.
/ APPLICANT: Schier, Robert
/ TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
/ TITLE OF INVENTION: Tumor Antigens
/ NUMBER OF SEQUENCES: 141
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/665,202
/ FILING DATE: 13-JUN-1996
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/000,238
/ FILING DATE: 14-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 60/000,250
/ FILING DATE: 15-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hunter, Tom
/ REGISTRATION NUMBER: 38,498
/ REFERENCE/DOCKET NUMBER: 02307E-061410
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 36:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 111 amino acids
/ TYPE: amino acid
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STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-665-202-36

Query Match 93.9%; Score 62; DB 2; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.0079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
|||:|||||||
Db 23 SGSSSNIGNNYVS 35

RESULT 5

US-08-665-202-42
Sequence 42, Application US/08665202
Patent No. 5977322

GENERAL INFORMATION:

APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 111 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-665-202-42

Query Match 93.9%; Score 62; DB 2; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.0079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
|||:|||||||
Db 23 SGSSSNIGNNYVS 35

RESULT 6

US-08-665-202-43

Sequence 43, Application US/08665202
Patent No. 5977322

GENERAL INFORMATION:

APPLICANT: Marks, James D.
APPLICANT: Schier, Robert
TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
TITLE OF INVENTION: Tumor Antigens
NUMBER OF SEQUENCES: 141
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/665,202
FILING DATE: 13-JUN-1996
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/000,238
FILING DATE: 14-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/000,250
FILING DATE: 15-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 02307E-061410

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:

LENGTH: 111 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-665-202-43

Query Match 93.9%; Score 62; DB 2; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.0079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
|||:|||||||

Db 23 SGSSSNIGNNYVS 35

RESULT 7

US-08-983-607-35

Sequence 35, Application US/08983607

Patent No. 6140470

GENERAL INFORMATION:

APPLICANT: Alan Garen
APPLICANT: Xiaohong Cai
TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
TITLE OF INVENTION: Bodies
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:

ADDRESSEE: Department of Molecular Biophysics

ADDRESSEE: and Biochemistry, Yale University

STREET: 266 Whitney Avenue

CITY: New Haven

STATE: Connecticut

COUNTRY: United States of America

ZIP: 06520-8114

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; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,607
; FILING DATE: April 27, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB96/01032
; FILING DATE: June 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Krinsky
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: OCR-679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-773-9544
; TELEFAX: 203-773-1183
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; DESCRIPTION: polypeptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens (melanoma patient immu-
; ORGANISM: nized with autologous tumor cells)
; INDIVIDUAL ISOLATE: peripheral blood lymphocytes
; IMMEDIATE SOURCE:
; LIBRARY: DM414 scFv antibodies obtained from
; LIBRARY: fuses fusion phage construct
; CLONE: V373
; FEATURE:
; NAME/KEY: light chain
US-08-983-607-35

Query Match 93.9%; Score 62; DB 3; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.0079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
Db 23 SGSSNIGNNYVS 35

RESULT 8
US-09-315-574-36
; Sequence 36, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,574
; FILING DATE: 20-MAY-99
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,202
; FILING DATE: 13-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; APPLICATION NUMBER: US/09/315,574

US-08-983-607-35
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,607
; FILING DATE: April 27, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB96/01032
; FILING DATE: June 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Krinsky
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: OCR-679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-773-9544
; TELEFAX: 203-773-1183
; INFORMATION FOR SEQ ID NO: 35:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: polypeptide
; DESCRIPTION: polypeptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens (melanoma patient immu-
; ORGANISM: nized with autologous tumor cells)
; INDIVIDUAL ISOLATE: peripheral blood lymphocytes
; IMMEDIATE SOURCE:
; LIBRARY: DM414 scFv antibodies obtained from
; LIBRARY: fuses fusion phage construct
; CLONE: V373
; FEATURE:
; NAME/KEY: light chain
US-08-983-607-35

Query Match 93.9%; Score 62; DB 4; Length 111;
Best Local Similarity 92.3%; Pred. No. 0.0079;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
Db 23 SGSSNIGNNYVS 35

RESULT 9
US-09-315-574-42
; Sequence 42, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,574
; FILING DATE: 20-MAY-99
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,202
; FILING DATE: 13-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; APPLICATION NUMBER: US/09/315,574

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; REGISTRATION NUMBER: 38,498
 ; REFERENCE/DOCKET NUMBER: 02307E-061411
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 42:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 111 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-09-315-574-42

Query Match 93.9%; Score 62; DB 4; Length 111;
 Best Local Similarity 92.3%; Pred. No. 0.0079;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
 |||:|||||||
 Db 23 SGSSNIGNNYVS 35

RESULT 10

US-09-315-574-43
 ; Sequence 43, Application US/09315574
 ; Patent No. 6512097
 ; GENERAL INFORMATION:
 ; APPLICANT: Marks, James D.
 ; APPLICANT: Schier, Robert
 ; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
 ; Tumor Antigens
 ; NUMBER OF SEQUENCES: 141
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
 ; STREET: Four Embarcadero Center, Suite 1100
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-4106

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/315,574
 ; FILING DATE: 20-MAY-99
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/000,238
 ; FILING DATE: 14-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/000,250
 ; FILING DATE: 15-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/665,202
 ; FILING DATE: 13-JUN-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hunter, Tom

; REGISTRATION NUMBER: 38,498
 ; REFERENCE/DOCKET NUMBER: 02307E-061411
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 43:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 111 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-09-315-574-43

Query Match 93.9%; Score 62; DB 4; Length 111;
 Best Local Similarity 92.3%; Pred. No. 0.0079;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
 |||:|||||||
 Db 23 SGSSNIGNNYVS 35

RESULT 11

US-08-665-202-39
 ; Sequence 39, Application US/08665202
 ; Patent No. 5977322
 ; GENERAL INFORMATION:
 ; APPLICANT: Marks, James D.
 ; APPLICANT: Schier, Robert
 ; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
 ; Tumor Antigens
 ; NUMBER OF SEQUENCES: 141
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Townsend and Townsend and Crew LLP
 ; STREET: Two Embarcadero Center, Eighth Floor
 ; CITY: San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94111-3834

; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/665,202
 ; FILING DATE: 13-JUN-1996
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/000,238
 ; FILING DATE: 14-JUN-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 60/000,250
 ; FILING DATE: 15-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Hunter, Tom

; REGISTRATION NUMBER: 38,498
 ; REFERENCE/DOCKET NUMBER: 02307E-061410
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 576-0200
 ; TELEFAX: (415) 576-0300
 ; INFORMATION FOR SEQ ID NO: 39:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 112 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-665-202-39

Query Match 93.9%; Score 62; DB 2; Length 112;
 Best Local Similarity 92.3%; Pred. No. 0.008;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13
 |||:|||||||
 Db 23 SGSSNIGNNYVS 35

RESULT 12

US-08-983-607-31
 ; Sequence 31, Application US/08983607
 ; Patent No. 6140470
 ; GENERAL INFORMATION:
 ; APPLICANT: Alan Garen

```

; APPLICANT: Xiaohong Cai
; TITLE OF INVENTION: Human Anti-Tumor Monoclonal Anti-
; bodies
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Department of Molecular Biophysics
; and Biochemistry, Yale University
; STREET: 266 Whitney Avenue
; CITY: New Haven
; STATE: Connecticut
; COUNTRY: United States of America
; ZIP: 06520-8114
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" 1.44 Mb diskette
; COMPUTER: IBM PC
; OPERATING SYSTEM: MS DOS
; SOFTWARE: Word Processing
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/983,607
; FILING DATE: April 27, 1998
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/IB96/01032
; FILING DATE: June 28, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Mary M. Krinsky
; REGISTRATION NUMBER: 32423
; REFERENCE/DOCKET NUMBER: OCR-679
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 203-773-9544
; TELEFAX: 203-773-1183
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 residues
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: polypeptide
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens (melanoma patient immu-
; ORGANISM: nized with autologous tumor cells)
; INDIVIDUAL ISOLATE: peripheral blood lymphocytes
; IMMEDIATE SOURCE:
; LIBRARY: DW414 scFv antibodies obtained from
; LIBRARY: fUSE5 fusion phage construct
; CLONE: V73
; FEATURE:
; NAME/KEY: light chain
; US-08-983-607-31

Query Match 93.9%; Score 62; DB 3; Length 112;
Best Local Similarity 92.3%; Pred. No. 0.008;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
DB 24 SGSSSNIGNNYVS 36

RESULT 13
US-09-025-7698-18
; Sequence 18, Application US/090257698
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries

```

```

; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-18

Query Match 93.9%; Score 62; DB 3; Length 112;
Best Local Similarity 92.3%; Pred. No. 0.008;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 SGSTSNIGNNYVS 13
DB 23 SGSSSNIGNNYVS 35

RESULT 14
US-09-315-574-39
; Sequence 39, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,574
; FILING DATE: 20-MAY-99
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995

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;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,202
; FILING DATE: 13-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061411
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-09-315-574-39

Query Match          93.9%; Score 62; DB 4; Length 112;
Best Local Similarity 92.3%; Pred. No. 0.008;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIIGNNVYS 13
Db 23 SGSSSNIIGNNVYS 35

RESULT 15
US-09-490-070A-18
; Sequence 18, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
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;
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-490-070A-18

Query Match          93.9%; Score 62; DB 4; Length 112;
Best Local Similarity 92.3%; Pred. No. 0.008;
Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIIGNNVYS 13
Db 23 SGSSSNIIGNNVYS 35

Search completed: October 14, 2005, 16:22:02
Job time : 26.5938 secs
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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:20:10 ; Search time 92.4219 Seconds
(without alignments)
58.615 Million cell updates/sec

Title: US-10-614-959-13
Perfect score: 66
Sequence: 1 SGSTSNTGNVYS 13

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1859788 seqs, 416717961 residues

Total number of hits satisfying chosen parameters: 1859788

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
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- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	66	100.0	240	10	US-09-880-748-1898 Sequence 1898, Ap
2	66	100.0	240	15	US-10-293-418-1898 Sequence 1898, Ap
3	66	100.0	242	18	US-10-981-692-24 Sequence 24, Appl
4	66	100.0	242	18	US-10-981-692-40 Sequence 40, Appl
5	66	100.0	243	10	US-09-880-748-1927 Sequence 1927, Ap
6	66	100.0	243	14	US-10-322-673-53 Sequence 53, Appl
7	66	100.0	243	15	US-10-293-418-1927 Sequence 1927, Ap
8	66	100.0	243	18	US-10-981-692-29 Sequence 29, Appl
9	66	100.0	243	18	US-10-981-692-33 Sequence 33, Appl
10	66	100.0	243	18	US-10-981-465-53 Sequence 53, Appl
11	66	100.0	243	18	US-10-981-621-53 Sequence 53, Appl

12	66	100.0	243	18	US-10-981-673-53 Sequence 53, Appl
13	66	100.0	243	18	US-10-981-691-53 Sequence 53, Appl
14	66	100.0	244	18	US-10-981-692-26 Sequence 26, Appl
15	66	100.0	245	10	US-09-880-748-1926 Sequence 1926, Ap
16	66	100.0	245	15	US-10-293-418-1926 Sequence 1926, Ap
17	66	100.0	245	15	US-10-293-418-3241 Sequence 3241, Ap
18	66	100.0	245	18	US-10-981-692-31 Sequence 31, Appl
19	66	100.0	245	18	US-10-981-692-36 Sequence 36, Appl
20	66	100.0	246	10	US-09-880-748-1913 Sequence 1913, Ap
21	66	100.0	246	10	US-09-880-748-1917 Sequence 1917, Ap
22	66	100.0	246	15	US-10-293-418-1913 Sequence 1913, Ap
23	66	100.0	246	15	US-10-293-418-1917 Sequence 1917, Ap
24	66	100.0	247	10	US-09-880-748-1443 Sequence 1443, Ap
25	66	100.0	247	10	US-09-880-748-1682 Sequence 1682, Ap
26	66	100.0	247	10	US-09-880-748-1707 Sequence 1707, Ap
27	66	100.0	247	10	US-09-880-748-1899 Sequence 1899, Ap
28	66	100.0	247	10	US-09-880-748-1928 Sequence 1928, Ap
29	66	100.0	247	10	US-09-880-748-1934 Sequence 1934, Ap
30	66	100.0	247	15	US-10-293-418-1443 Sequence 1443, Ap
31	66	100.0	247	15	US-10-293-418-1682 Sequence 1682, Ap
32	66	100.0	247	15	US-10-293-418-1707 Sequence 1707, Ap
33	66	100.0	247	15	US-10-293-418-1899 Sequence 1899, Ap
34	66	100.0	247	15	US-10-293-418-1928 Sequence 1928, Ap
35	66	100.0	247	15	US-10-293-418-1934 Sequence 1934, Ap
36	66	100.0	247	17	US-10-935-290-46 Sequence 46, Appl
37	66	100.0	247	17	US-10-935-290-88 Sequence 88, Appl
38	66	100.0	247	18	US-10-981-692-27 Sequence 27, Appl
39	66	100.0	247	18	US-10-981-692-37 Sequence 37, Appl
40	66	100.0	247	20	US-11-046-857-44 Sequence 44, Appl
41	66	100.0	248	18	US-10-981-692-39 Sequence 39, Appl
42	66	100.0	249	10	US-09-880-748-1419 Sequence 1419, Ap
43	66	100.0	249	10	US-09-880-748-1618 Sequence 1618, Ap
44	66	100.0	249	10	US-09-880-748-2049 Sequence 2049, Ap
45	66	100.0	249	15	US-10-293-418-1419 Sequence 1419, Ap

ALIGNMENTS

RESULT 1

US-09-880-748-1898
; Sequence 1898, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1898
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1898

Query Match 100.0%; Score 66; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNTGNVYS 13
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Db 153 SGSTSNIGNNYVS 165

RESULT 2

US-10-293-418-1898
; Sequence 1898, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIORITY FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1898
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-293-418-1898

Query Match 100.0%; Score 66; DB 15; Length 240;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13

Db 153 SGSTSNIGNNYVS 165

RESULT 3

US-10-981-692-24
; Sequence 24, Application US/10981692
; Publication No. US2005016377A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B

; FILE REFERENCE: PF590P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; PRIORITY FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N015E08 scFv

US-10-981-692-24

Query Match 100.0%; Score 66; DB 18; Length 242;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13

Db 154 SGSTSNIGNNYVS 166

RESULT 4

US-10-981-692-40
; Sequence 40, Application US/10981692
; Publication No. US2005016377A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B

; FILE REFERENCE: PF590P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; PRIORITY FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N015D10 scFv

US-10-981-692-40

Query Match 100.0%; Score 66; DB 18; Length 242;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13

Db 154 SGSTSNIGNNYVS 166

RESULT 5

US-09-880-748-1927
; Sequence 1927, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIORITY FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1927
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-880-748-1927

Query Match 100.0%; Score 66; DB 10; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNYVS 13

Db 155 SGSTSNIGNNYVS 167


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; ORGANISM: Homo sapiens
US-10-293-418-1927

Query Match      100.0%; Score 66; DB 15; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SGSTSNIIGNNVYS 13
Db      155 SGSTSNIIGNNVYS 167

RESULT 8
US-10-981-692-29
; Sequence 29, Application US/10981692
; Publication No. US20050163777A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PF590P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N024E07 scFv
US-10-981-692-29

Query Match      100.0%; Score 66; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SGSTSNIIGNNVYS 13
Db      155 SGSTSNIIGNNVYS 167

RESULT 9
US-10-981-692-33
; Sequence 33, Application US/10981692
; Publication No. US20050163777A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PF590P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N023E01 scFv
US-10-981-692-33

Query Match      100.0%; Score 66; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SGSTSNIIGNNVYS 13
Db      155 SGSTSNIIGNNVYS 167

RESULT 6
US-10-322-673-53
; Sequence 53, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: PF585
; CURRENT APPLICATION NUMBER: US/10/322,673
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; NUMBER OF SEQ ID NOS: 72
; SEQ ID NO 53
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM085C11 scFv
US-10-322-673-53

Query Match      100.0%; Score 66; DB 14; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SGSTSNIIGNNVYS 13
Db      155 SGSTSNIIGNNVYS 167

RESULT 7
US-10-293-418-1927
; Sequence 1927, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1927
; LENGTH: 243
; TYPE: PRT
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QY      1 SGSTSNIGNNYVS 13
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Db      155 SGSTSNIGNNYVS 167

RESULT 10
US-10-981-465-53
; Sequence 53, Application US/10981465
; Publication No. US20050214205A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585P1
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/608,386
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 53
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM085C11 scFv
US-10-981-621-53

Query Match      100.0%; Score 66; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGSTSNIGNNYVS 13
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Db      155 SGSTSNIGNNYVS 167

RESULT 12
US-10-981-673-53
; Sequence 53, Application US/10981673
; Publication No. US20050214207A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585P1D2
; CURRENT APPLICATION NUMBER: US/10/981,673
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/608,386
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 53
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM085C11 scFv
US-10-981-621-53

Query Match      100.0%; Score 66; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 SGSTSNIGNNYVS 13
      |||||
Db      155 SGSTSNIGNNYVS 167

RESULT 11
US-10-981-621-53
; Sequence 53, Application US/10981621
; Publication No. US20050214206A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585P1D1
; CURRENT APPLICATION NUMBER: US/10/981,621
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/608,386
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
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Query Match 100.0%; Score 66; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNVYS 13
Db 155 SGSTSNIGNNVYS 167

RESULT 13

US-10-981-691-53
; Sequence 53, Application US/10981691
; Publication No. US20050214208A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: PF585P1D3
; CURRENT APPLICATION NUMBER: US/10/981,691
; PRIOR FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: 60/608,386
; PRIOR FILING DATE: 2004-09-10
; PRIOR APPLICATION NUMBER: PCT/US04/013900
; PRIOR FILING DATE: 2004-05-05
; PRIOR APPLICATION NUMBER: 60/468,092
; PRIOR FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: 60/495,140
; PRIOR FILING DATE: 2003-08-15
; PRIOR APPLICATION NUMBER: 10/322,673
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/369,877
; PRIOR FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/384,828
; PRIOR FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: 60/396,591
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/403,370
; PRIOR FILING DATE: 2002-08-15
; PRIOR APPLICATION NUMBER: 60/425,737
; PRIOR FILING DATE: 2002-11-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 76
; SEQ ID NO 53
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: CM085C11 scFv

US-10-981-691-53

Query Match 100.0%; Score 66; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNVYS 13
Db 155 SGSTSNIGNNVYS 167

RESULT 14

US-10-981-692-26
; Sequence 26, Application US/10981692
; Publication No. US20050163777A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PF590P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30

; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N024D01 scFv
US-10-981-692-26

Query Match 100.0%; Score 66; DB 18; Length 244;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNVYS 13
Db 156 SGSTSNIGNNVYS 168

RESULT 15

US-09-880-748-1926
; Sequence 1926, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
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; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1926
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1926

Query Match 100.0%; Score 66; DB 10; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SGSTSNIGNNVYS 13
Db 157 SGSTSNIGNNVYS 169

Search completed: October 14, 2005, 17:00:43
Job time : 92.4219 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 15:51:19 ; Search time 53.8125 Seconds
(without alignments)
50.310 Million cell updates/sec

Title: US-10-614-959-14

Perfect score: 35

Sequence: 1 DVSKRPS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_16Dec04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	100.0	7	3	AA79072 Anti-fact
2	35	100.0	99	7	ADJ80338
3	35	100.0	109	4	AAU02544
4	35	100.0	110	3	AA79060 Human ant
5	35	100.0	110	4	AAU02558
6	35	100.0	110	4	AAU02612
7	35	100.0	110	4	AAU02627
8	35	100.0	110	4	AAU02629
9	35	100.0	111	2	AAW19883
10	35	100.0	111	4	AAU02542
11	35	100.0	111	4	AAU02551
12	35	100.0	111	4	AAU02585
13	35	100.0	111	7	ADK17416
14	35	100.0	111	8	ADG42838 scFv Ab12
15	35	100.0	214	8	ABM85072 Human dia
16	35	100.0	236	8	ABM85084 Human dia
17	35	100.0	240	5	ADP45887 Human Bly
18	35	100.0	240	7	ADG96714 Single ch
19	35	100.0	241	5	ABP46044 Human Bly
20	35	100.0	241	7	ADG96871 Single ch
21	35	100.0	242	8	ADG34301 Neurokini
22	35	100.0	242	8	ADG34317 Neurokini
23	35	100.0	243	5	ADP45916 Human Bly
24	35	100.0	243	7	ADG96743 Single ch
25	35	100.0	243	8	ADG34310 Neurokini

26	35	100.0	243	8	ADG34306	Adg34306 Neurokini
27	35	100.0	244	8	ADG34303	Adg34303 Neurokini
28	35	100.0	245	5	ABP45915	Adp45915 Human Bly
29	35	100.0	245	7	ADG96742	Adg96742 Single ch
30	35	100.0	245	7	ADG98057	Adg98057 TNF proli
31	35	100.0	245	8	ADG83862	Adg83862 Chemokine
32	35	100.0	245	8	ADG34308	Adg34308 Neurokini
33	35	100.0	245	8	ADG34313	Adg34313 Neurokini
34	35	100.0	246	5	ABP45902	Adp45902 Human Bly
35	35	100.0	246	5	ABP45906	Adp45906 Human Bly
36	35	100.0	246	7	ADG96733	Adg96733 Single ch
37	35	100.0	246	7	ADG96729	Adg96729 Single ch
38	35	100.0	246	8	ADG83872	Adg83872 Chemokine
39	35	100.0	247	5	ABP45671	Adp45671 Human Bly
40	35	100.0	247	5	ABP45674	Adp45674 Human Bly
41	35	100.0	247	5	ABP45432	Adp45432 Human Bly
42	35	100.0	247	5	ABP45923	Adp45923 Human Bly
43	35	100.0	247	5	ABP45917	Adp45917 Human Bly
44	35	100.0	247	5	ABP45696	Adp45696 Human Bly
45	35	100.0	247	5	ABP45888	Adp45888 Human Bly

ALIGNMENTS

RESULT 1
AA79072
ID AA79072 standard; peptide; 7 AA.
XX
AC AA79072;
XX
DT 12-JUN-2000 (first entry)
XX
DE Anti-factor IX/IXa antibody L chain V domain CDR2 amino acid sequence.
XX
KW Complementarity determining region 2; CDR2; antibody; Gla domain;
KW factor IX/IXa; blood coagulation; deep venous thrombosis; light chain;
KW arterial thrombosis; unstable angina; post myocardial infarction;
KW coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;
KW percutaneous transluminal coronary angioplasty; PTCA; inflammation;
KW septic shock; hypotension; adult respiratory distress syndrome; ARDS;
KW arterial fibrillation; disseminated intravascular coagulopathy; DIC.
XX
OS Homo sapiens.
XX
PN WO200012562-A1.
XX
PD 09-MAR-2000.

XX 26-AUG-1999; 99WO-US019453.
XX 28-AUG-1998; 98US-0098233P.
PR 03-MAR-1999; 99US-0122767P.
XX (GETH) GENENTECH INC.
XX Adams CW, Devaux B, Eaton DL, Hass PE, Judice JK, Kirchhofer D;
PI Suggett S;
XX WPI; 2000-256595/22.
DR Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-
XX carboxyglutamic acid domains useful as anti-coagulant in thrombosis,
XX stroke, and post myocardial infarction.
PT Claim 8; Fig 2; 84pp; English.
XX This sequence represents a complementarity determining region 2 (CDR2) of
XX the light chain variable domain of a human anti-factor IX/IXa Gla domain
XX antibody. Factor IXa is a vitamin K dependent plasma serine protease that
XX participates in the blood coagulation pathways. The Gla domain of factor
XX IXa and its zymogen factor IX contains important structural determinants
XX for interaction with high affinity binding sites on vascular endothelial

CC cells and platelets. Compositions comprising the antibodies are used for
 CC the treatment or prophylaxis of thrombotic or coagulopathic diseases or
 CC disorders in a mammal for which inhibiting a FIX/FIXa mediated event is
 CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
 CC angina, post myocardial infarction, post surgical thrombosis, coronary
 CC artery bypass graft (CABG), percutaneous transluminal coronary
 CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
 CC inflammation, septic shock, hypotension, adult respiratory distress
 CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
 CC coagulopathy (DIC)

XX SQ Sequence 7 AA;

Query Match 100.0%; Score 35; DB 3; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
 |||||
 Db 1 DVSKRPS 7

RESULT 2

ADJ80338
 ID ADJ80338 standard; protein; 99 AA.

XX AC ADJ80338;

XX DT 06-MAY-2004 (first entry)

XX DE Vlamda gene locus antibody amino acid sequence #7.

XX KW hybrid antibody; antibody; framework region; homology; immunogenicity.

XX OS Homo sapiens.

XX PN WO2003048321-A2.

XX PD 12-JUN-2003.

XX PF 03-DEC-2002; 2002WO-US038450.

XX PR 03-DEC-2001; 2001US-0336591P.

XX PA (ALEX-) ALEXION PHARM INC.

XX PI Rother R, Wu D;

XX PS WPI; 2003-513753/48.

XX PT Producing a hybrid antibody or hybrid antibody fragment by operatively
 XX linking the selected framework sequences to one or more complementarity
 XX determining regions of the initial antibody.

XX PS Disclosure; SEQ ID NO 98; 77pp; English.

XX CC The invention relates to a method of producing a hybrid antibody or
 CC hybrid antibody fragment by: (i) providing an initial antibody having
 CC specificity for a target; (ii) determining the sequence of a variable
 CC region of the initial antibody; (iii) selecting a first component of the
 CC variable region consisting of FR1, FR2, FR3 and FR4; (iv) comparing the
 CC sequence of the first component to sequences contained in a reference
 CC database of antibody sequences or antibody fragment sequences from a
 CC target species; (v) selecting a sequence from an antibody in the database
 CC which demonstrates a high degree of homology to the first component; (vi)
 CC selecting a second component of the variable region which is different
 CC than the first component, the second component selected from the group
 CC consisting of FR1, FR2, FR3 and FR4; (vii) comparing the sequence of the
 CC second component to sequences contained in a reference database of
 CC antibody sequences or antibody fragment sequences from the target species
 CC ; (viii) selecting a sequence from the database which demonstrates a high
 CC degree of homology to the second component and which is from a different
 CC antibody than the selected antibody; and (ix) operatively linking the

CC selected framework sequences to one or more complementarity determining
 CC regions (CDRs) of the initial antibody to produce a hybrid antibody or
 CC hybrid antibody fragment. The method is useful for producing a hybrid
 CC antibody or hybrid antibody fragment (claimed). The antibody and
 CC fragments are useful for therapeutic and diagnostic purposes. The method
 CC uses entire framework regions from a single antibody variable heavy or
 CC variable light chain to receive the CDRs. This produces antibodies that
 CC are highly homologous and exhibit reduced immunogenicity while
 CC maintaining an optimum binding profile. This sequence represents the
 CC amino acid sequence of an antibody from the Vlamda gene locus.

XX SQ Sequence 99 AA;

Query Match 100.0%; Score 35; DB 7; Length 99;
 Best Local Similarity 100.0%; Pred. No. 5.4;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
 |||||
 Db 52 DVSKRPS 58

RESULT 3

AAU02544
 ID AAU02544 standard; protein; 109 AA.

XX AC AAU02544;

XX DT 29-AUG-2001 (first entry)

XX DE Anti-adipocyte monoclonal antibody light chain, FAT 31.

XX KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KW heart disease; complementarity determining region; CDR.

XX OS Homo sapiens.

XX PN WO200127279-A1.

XX PD 19-APR-2001.

XX PF 11-OCT-2000; 2000WO-GB003900.

XX PR 12-OCT-1999; 99US-0158812P.

XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Edwards BM, Main SH, Vaughan TJ;

XX PS WPI; 2001-282031/29.

XX DR N-PSDB; AAS03444.

XX PT Panel of specific binding members of antibody molecules which bind to
 XX whole adipocytes is used in the treatment of obesity and obesity related
 XX diseases.

XX PS Claim 1; Page 120; 182pp; English.

XX CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies

CC for different types of fat deposits can also be produced e.g. intra-abdominal fat associated with heart disease

XX Sequence 109 AA;

Query Match 100.0%; Score 35; DB 4; Length 109;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
| | | | |
Db 51 DVSKRPS 57

RESULT 4

ID AAY96060 standard; protein; 110 AA.

XX AAY96060;

XX 05-DEC-2000 (first entry)

XX Human anti-DAF antibody LU30 light chain variable region.

XX LU30; human; antibody; VL domain; decay accelerating factor; DAF;
XX phage display; subtractive panning; lung cancer; lung carcinoma;
XX lung adenocarcinoma; therapy; diagnosis.

XX Homo sapiens.

XX Key Location/Qualifiers

XX 23. .36

XX /label= CDRI

XX /note= "complementarity determining region I"

XX 25. .35

XX /note= "hypervariable loop region"

XX 52. .58

XX /label= CDRII

XX /note= "complementarity determining region II"

XX 52. .54

XX /note= "hypervariable loop residues"

XX 91. .100

XX /label= CDRIII

XX /note= "complementarity determining region III"

XX 93. .99

XX /note= "hypervariable loop residues"

XX WO200052054-A2.

XX 08-SEP-2000.

XX 29-FEB-2000; 2000WO-US005352.

XX 01-MAR-1999; 99US-0122262P.

XX (GETH) GENENTECH INC.

XX Carter PJ, Ridgway JB;

XX WPI; 2000-594169/56.

XX Making antibodies (e.g. anti-decay accelerating factor antibody) for
XX diagnosing or treating e.g. lung cancer comprises identifying an antigen
XX that is differentially expressed on the surface of two or more distinct
XX cell populations.

XX Disclosure; Fig 5A; 52pp; English.

XX The present sequence is that of the light chain variable region (VL) of
XX the anti-decay accelerating factor (DAF) human antibody LU30. The VH
XX region is given in AAY0603. LU30 has a binding affinity (Kd) for DAF of
XX about 13 nM. It was produced using a novel method for making antibodies
XX which can be used for cancer diagnosis or therapy. The method comprises:

CC (a) binding an antibody phage from a naive antibody phage library to a
CC live cancer cell; (b) selecting an antibody phage or antibody which binds
CC selectively to the live cancer cell; and (c) identifying an antigen to
CC which the antibody phage or antibody binds. To obtain LU30, a human scFv
CC library was used to search for tumour-associated antigens by panning the
CC lung adenocarcinoma cell line 1264, and counter-selecting with a non-
CC tumour bronchial epithelial cell line, BEAS-2B. The invention also
CC describes a method for identifying an antigen which is differentially
CC expressed on the surface of 2 or more distinct cell populations. The anti-
CC -DAF human antibody, or a composition comprising the antibody, is useful
CC for in vivo cancer diagnosis or therapy. In particular, the antibody is
CC useful for diagnosing or treating lung cancer; e.g. small-cell lung
CC cancer, non-small cell lung cancer, large cell lung carcinoma, lung
CC adenocarcinoma, or squamous cell lung carcinoma (all claimed)

XX SQ Sequence 110 AA;

Query Match 100.0%; Score 35; DB 3; Length 110;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7

Db 52 DVSKRPS 58

RESULT 5

ID AAU02558

XX AAU02558 standard; protein; 110 AA.

XX AAU02558;

XX 29-AUG-2001 (first entry)

XX Anti-adipocyte monoclonal antibody light chain, FAT 44.

XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;

XX heart disease; complementarity determining region; CDR.

XX Homo sapiens.

XX WO200127279-A1.

XX 19-APR-2001.

XX 11-OCT-2000; 2000WO-GB003900.

XX 12-OCT-1999; 99US-0158812P.

XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Edwards EM, Main SH, Vaughan TJ;

XX WPI; 2001-282031/29.

XX N-PSDB; AAS03458.

XX Panel of specific binding members of antibody molecules which bind to
XX whole adipocytes is used in the treatment of obesity and obesity related
XX diseases.
XX Claim 1; Page 128-129; 182pp; English.
XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
XX sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
XX and heavy chain complementarity determining regions (CDR) of the
XX invention. The antibodies can be used in the treatment of obesity and
XX obesity related diseases. The antibodies can be used to deliver drugs or
XX pro-drugs directly to the fat mass of an obese patient or the antibody
XX can be used as a therapeutic itself. Antibodies binding specifically to
XX adipocytes can be used to activate the immune system to destroy the cells
XX by complement mediated lysis. The antibodies may be labeled with a
XX detectable label such as radiolabel, fluorescent or chemical group and
XX used in methods of diagnosis in human subjects e.g. to determine the

CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-
 CC abdominal fat associated with heart disease
 XX
 SQ Sequence 110 AA;

Query Match 100.0%; Score 35; DB 4; Length 110;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
 |||||
 Db 51 DVSKRPS 57

RESULT 6

AAU02612
 ID AAU02612 standard; protein; 110 AA.

XX AC AAU02612;

XX DT 29-AUG-2001 (first entry)

XX DE Anti-adipocyte monoclonal antibody light chain, FAT 99.

XX KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KW heart disease; complementarity determining region; CDR.

XX OS Homo sapiens.

XX PN WO200127279-A1.

XX PD 19-APR-2001.

XX PF 11-OCT-2000; 2000WO-GB003900.

XX PR 12-OCT-1999; 99US-0158812P.

XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Edwards BM, Main SH, Vaughan TJ;

XX DR WPI; 2001-282031/29.

XX DR N-PSDB; AAS03512.

XX PT Panel of specific binding members of antibody molecules which bind to
 PT whole adipocytes is used in the treatment of obesity and obesity related
 PT diseases.

XX PS Claim 1; Page 163; 182pp; English.

XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-
 CC abdominal fat associated with heart disease

XX SQ Sequence 110 AA;

Query Match 100.0%; Score 35; DB 4; Length 110;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
 |||||
 Db 51 DVSKRPS 57

RESULT 7

AAU02627
 ID AAU02627 standard; protein; 110 AA.

XX AC AAU02627;

XX DT 29-AUG-2001 (first entry)

XX DE Anti-adipocyte monoclonal antibody light chain, FAT 112.

XX KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KW heart disease; complementarity determining region; CDR.

XX OS Homo sapiens.

XX PN WO200127279-A1.

XX PD 19-APR-2001.

XX PF 11-OCT-2000; 2000WO-GB003900.

XX PR 12-OCT-1999; 99US-0158812P.

XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Edwards BM, Main SH, Vaughan TJ;

XX DR WPI; 2001-282031/29.

XX DR N-PSDB; AAS03527.

XX PT Panel of specific binding members of antibody molecules which bind to
 PT whole adipocytes is used in the treatment of obesity and obesity related
 PT diseases.

XX PS Claim 1; Page 172; 182pp; English.

XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-
 CC abdominal fat associated with heart disease

XX SQ Sequence 110 AA;

Query Match 100.0%; Score 35; DB 4; Length 110;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
 |||||
 Db 51 DVSKRPS 57

RESULT 8

AAU02629
ID AAU02629 standard; protein; 110 AA.

XX AC AAU02629;

XX DT 29-AUG-2001 (first entry)

XX DE Anti-adipocyte monoclonal antibody light chain, FAT 113.

XX KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
heart disease; complementarity determining region; CDR.

XX OS Homo sapiens.

XX PN WO200127279-A1.

XX PD 19-APR-2001.

XX PF 11-OCT-2000; 2000WO-GB003900.

XX PR 12-OCT-1999; 99US-0158812P.

XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Edwards BM, Main SH, Vaughan TJ;

XX DR WPI; 2001-282031/29.

XX DR N-PSDB; AAS03529.

XX PT Panel of specific binding members of antibody molecules which bind to
whole adipocytes is used in the treatment of obesity and obesity related
diseases.

XX PS Claim 1; Page 173; 182pp; English.

XX CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
and heavy chain complementarity determining regions (CDR) of the
invention. The antibodies can be used in the treatment of obesity and
obesity related diseases. The antibodies can be used to deliver drugs or
pro-drugs directly to the fat mass of an obese patient or the antibody
can be used as a therapeutic itself. Antibodies binding specifically to
adipocytes can be used to activate the immune system to destroy the cells
by complement mediated lysis. The antibodies may be labeled with a
detectable label such as radiolabel, fluorescent or chemical group and
used in methods of diagnosis in human subjects e.g. to determine the
presence of adipocyte antigen on the surface of an adipocyte to detect or
determine the presence or level of adipocytes in a cell or tissue sample.
The antibodies can be used as an alternative means of treatment for obese
patients other than undergoing surgery to remove excess fat. Antibodies
for different types of fat deposits can also be produced e.g. intra-
abdominal fat associated with heart disease

XX SQ Sequence 110 AA;

Query Match 100.0%; Score 35; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7

Db 51 DVSKRPS 57

RESULT 9

AAW19883

ID AAW19883 standard; protein; 111 AA.

XX AC AAW19883;

XX AC

DT 07-DEC-1997 (first entry)

XX CEA-specific antibody CEA1, CEA2, CEA3 VL sequence.

XX KW Carcinoembryonic antigen; CEA; human; antibody; scFv; tumour marker;
lung cancer; breast cancer; colon cancer; adenocarcinoma; diagnosis.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT 23..35

XX FT /label= CDR1

XX FT /note= "complementarity determining region 1"

XX FT 50..56

XX FT /label= CDR2

XX FT /note= "complementarity determining region 2"

XX FT 90..100

XX FT /label= CDR3

XX FT /note= "complementarity determining region 3"

XX PN WO9720932-A1.

XX PD 12-JUN-1997.

XX PF 09-DEC-1996; 96WO-GB003043.

XX PR 07-DEC-1995; 95GB-00025004.

XX PR 23-MAY-1996; 96GB-00010824.

XX PR 11-OCT-1996; 96GB-00021295.

XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Osbourn JK, Allen DJ, McCafferty JG;

XX DR WPI; 1997-319779/29.

XX DR N-PSDB; AAT72133.

XX PT Specific binding members for human carcinoembryonic antigen - bind to the
A3-B3 extracellular domain of hCEA and are substantially non-cross-
reactive with human liver cells; used for diagnosing cancer.

XX PS Claim 14; Fig 1b; 128pp; English.

XX CC This polypeptide sequence comprises the light chain variable region (VL)
of human carcinoembryonic antigen (hCEA)-specific antibodies CEA1, CEA2
and CEA3. VH (AAT72126-32) and VL (AAT72133-35) gene sequences were
obtained for anti-hCEA antibodies CEA1-CEA7 (see AAW19876-85). A claimed
specific binding member (A) comprises an hCEA specific antibody antigen
binding domain that has a dissociation constant for hCEA of less than 1 x
10⁻⁸ M, is non-cross-reactive with human liver cells, and
preferentially binds to the A3-B3 extracellular domain of hCEA and/or to
cell-associated hCEA over hCEA over soluble hCEA. Preferred (A) include
pairings of VH and VL sequences from CEA1-7, or their CDR sequences, as
well as CEA6 VH and VL variants. (A) is used to detect cells expressing
hCEA, in vivo or in vitro, especially tumour cells for diagnosing cancer,
e.g. adenocarcinoma of the colon, lung or breast

XX SQ Sequence 111 AA;

Query Match 100.0%; Score 35; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7

Db 51 DVSKRPS 57

RESULT 10

AAU02542

ID AAU02542 standard; protein; 111 AA.

XX AC AAU02542;

```

XX 29-AUG-2001 (first entry)
XX Anti-adipocyte monoclonal antibody light chain, FAT 30.
DE
XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.
XX
XX Homo sapiens.
OS
XX WO200127279-A1.
PN
XX 19-APR-2001.
PD
XX 11-OCT-2000; 2000WO-GB003900.
PF
XX 12-OCT-1999; 99US-0158812P.
PR
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PA
XX Edwards BM, Main SH, Vaughan TJ;
PI
XX WPI; 2001-282031/29.
DR
XX N-PSDB; AAS03442.
DR
XX Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.
PT
XX Claim 1; Page 118-119; 182pp; English.
PS
XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease
XX Sequence 111 AA;
SQ
Query Match 100.0%; Score 35; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 51 DVSKRPS 57

RESULT 11
AAU02551
ID AAU02551 standard; protein; 111 AA.
XX
AC AAU02551;
XX
XX 29-AUG-2001 (first entry)
XX Anti-adipocyte monoclonal antibody light chain, FAT 37.
DE
XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.
XX
XX

```

```

OS Homo sapiens.
XX WO200127279-A1.
PN
XX 19-APR-2001.
PD
XX 11-OCT-2000; 2000WO-GB003900.
PF
XX 12-OCT-1999; 99US-0158812P.
PR
XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PA
XX Edwards BM, Main SH, Vaughan TJ;
PI
XX WPI; 2001-282031/29.
DR
XX N-PSDB; AAS03451.
DR
XX Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.
PT
XX Claim 1; Page 124; 182pp; English.
PS
XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease
XX Sequence 111 AA;
SQ
Query Match 100.0%; Score 35; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 52 DVSKRPS 58

RESULT 12
AAU02585
ID AAU02585 standard; protein; 111 AA.
XX
AC AAU02585;
XX
XX 29-AUG-2001 (first entry)
XX Anti-adipocyte monoclonal antibody light chain, FAT 72.
DE
XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.
XX
XX Homo sapiens.
OS
XX WO200127279-A1.
PN
XX 19-APR-2001.
PD
XX 11-OCT-2000; 2000WO-GB003900.
PF
XX

```

PR 12-OCT-1999; 99US-0159812P.
 XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX Edwards BM, Main SH, Vaughan TJ;
 XX WPI; 2001-282031/29.
 DR N-PSDB; AAS03485.
 XX
 XX Panel of specific binding members of antibody molecules which bind to
 PT whole adipocytes is used in the treatment of obesity and obesity related
 PT diseases.
 XX
 XX Claim 1; Page 146; 182pp; English.
 XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-
 CC abdominal fat associated with heart disease
 XX
 XX Sequence 111 AA;
 SQ
 Query Match 100.0%; Score 35; DB 4; Length 111;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DVSKRPS 7
 Db 51 DVSKRPS 57
 RESULT 13
 ADK17416
 ID ADK17416 standard; protein; 111 AA.
 XX
 XX ADK17416;
 DT 06-MAY-2004 (first entry)
 XX
 DE Anti-human CXCR4 loop 6 scFv antibody V1 region.
 XX
 XX anti-HIV; cytostatic; virucide; single chain antibody; antibody; yeast;
 KW HIV; cancer; CCR5.
 XX
 XX Synthetic.
 OS
 XX WO2003066830-A2.
 PN
 XX 14-AUG-2003.
 PD
 XX 07-FEB-2003; 2003WO-US003763.
 PF
 XX 08-FEB-2002; 2002US-00071866.
 XX 08-FEB-2002; 2002US-00072031.
 PR 25-APR-2002; 2002US-00133978.
 XX
 XX (GENE-) GENETASTIX CORP.
 PA
 XX Hua S, Pauling MH, Zhu L;
 XX
 XX WPI; 2004-051479/05.
 DR

DR WPI; 2003-731501/69.
 XX
 XX Selecting an scFv against a peptide target by expressing a target fusion
 PT protein having a DNA binding domain or activation domain of a
 PT transcription activator, useful for diagnosing, preventing and/or
 PT treating HIV infection and cancer.
 XX
 XX Claim 123; SEQ ID NO 61; 150pp; English.
 PS
 XX
 XX The invention relates to a method of selecting a single chain antibody
 CC (scFv) against a peptide target in a yeast by expressing a library of
 CC scFv fusion proteins in yeast cells, expressing a target fusion protein
 CC in the yeast cells expressing the scFv fusion proteins having either the
 CC DNA binding domain or the activation domain of the transcription
 CC activator which is not comprised in the scFv fusion proteins, and a
 CC target peptide, and selecting those yeast cells in which a reporter gene
 CC is expressed. Each scFv fusion protein comprises either an activation
 CC domain or a DNA binding domain of a transcription activator and a scFv
 CC having a heavy chain of a variable region (VH) of antibody whose sequence
 CC varies within the library, a light chain of a variable region (VL) of
 CC antibody whose sequence varies within the library independently of the VH
 CC and a linker peptide which links the VH and VL. The expression of the
 CC reporter gene is activated by a reconstituted transcriptional activator
 CC formed by binding of the scFv fusion protein to the target fusion
 CC protein. The methods and compositions of the present invention are useful
 CC for preventing and/or treating HIV infection and cancer. This sequence
 CC corresponds to the V1 region of an anti-human CXCR4 loop 6 antibody gene
 CC and used to generate the scFv antibody of the invention.
 XX
 XX Sequence 111 AA;
 SQ
 Query Match 100.0%; Score 35; DB 7; Length 111;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 DVSKRPS 7
 Db 52 DVSKRPS 58
 RESULT 14
 ADG42838
 ID ADG42838 standard; protein; 111 AA.
 XX
 XX ADG42838;
 DT 26-FEB-2004 (first entry)
 XX
 DE scFv Ab124 light chain variable region.
 XX
 XX HIV infection; HIV type 1; HIV type 2; cancer; breast; prostate; liver;
 KW renal; lung; skin; ovarian; cervical; brain; thyroid; stomach; colon;
 KW lymphoma; leukaemia; pancreas; chemokine receptor; antibody.
 XX
 XX Synthetic.
 OS
 XX US2003206909-A1.
 PN
 XX 06-NOV-2003.
 PD
 XX 07-FEB-2003; 2003US-00360828.
 PF
 XX 08-FEB-2002; 2002US-00071866.
 PR 08-FEB-2002; 2002US-00072301.
 PR 25-APR-2002; 2002US-00133978.
 XX
 XX (HUAS/) HUA S.
 PA (PAUL/) PAULING M H.
 PA (ZHUL/) ZHU L.
 XX
 XX Hua S, Pauling MH, Zhu L;
 XX
 XX WPI; 2004-051479/05.
 DR

DR N-PSDB; ADG42836.
 XX Antibody binding loop of human chemokine receptor useful for the
 PT treatment of HIV infection and cancer.
 PT
 XX Claim 6; SEQ ID NO 61; 74pp; English.
 XX
 CC The invention relates to an antibody that binds to loop 6 of human
 CC chemokine receptor (CXCR4). The antibody is useful in the treatment or
 CC prevention of HIV infection (e.g. HIV type 1 and HIV type 2) and cancer
 CC of (e.g. breast, prostate, liver, renal, lung, skin, ovarian, cervical,
 CC brain, thyroid, stomach, colon, lymphoma, leukaemia and pancreas cancer
 CC cells), for screening drugs, for diagnosing disease or condition
 CC associated with interaction with chemokine receptor. The present sequence
 CC is used in the exemplification of the present invention.
 XX
 XX Sequence 111 AA;
 SQ
 Query Match 100.0%; Score 35; DB 8; Length 111;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVSKRPS 7
 |||||
 DB 52 DVSKRPS 58
 RESULT 15
 ABM85072
 ID ABM85072 standard; protein; 214 AA.
 XX
 AC ABM85072;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Human diagnostic and therapeutic pprotein SEQ ID NO:5321.
 XX
 DE gene therapy; human diagnostic and therapeutic polynucleotide; dithp.
 KW
 XX Homo sapiens.
 OS
 XX WO2004023973-A2.
 PN
 XX 25-MAR-2004.
 PD
 XX
 XX 12-SEP-2003; 2003WO-US028227.
 PF
 XX 12-SEP-2002; 2002US-0410259P.
 PR
 XX 12-SEP-2002; 2002US-0410260P.
 PR
 XX (INCY-) INCYTE CORP.
 PA
 XX Schmidt JP, Wright RJ, Bruns CM, Marjanovic MM, Shen F;
 PI Hartshorne TA, Suchorolski MT, Altus CM, Pitts SJ, Elder LV;
 PI Mooney EM, Delegeane AM, Panesar IS, Banville SC, Reddy TP;
 PI Stevens KA, Blanchard JL, Panzer SR, Wang X, Au AP, Gerstin EH;
 PI Peralta CH, Anderson SB, Rioux P, Shen EJ, Wu MC, Stuve LL;
 PI Lagace RE, Spiro PA, Stewart EA, Wingrove J, Vitt UA, Kirton ES;
 PI Xu Y, Kwong M, Policky JL, Hurwitz BL, Ma Y, Jackson JL, Gietzen D;
 PI Patury S, Shi X, Suarez CJ;
 XX
 XX WPI: 2004-329368/30.
 DR N-PSDB; ACN43724.
 DR
 XX
 XX New diagnostic and therapeutic polynucleotides and polypeptides, useful
 PT in diagnosing a condition, disease or disorder associated with human
 PT molecules, e.g. autoimmune or inflammatory disorders, in gene therapy or
 PT in gene mapping.
 PT
 XX Claim 27; Page; 190pp; English.
 XX
 XX The invention relates to novel diagnostic and therapeutic polynucleotides
 CC selected from one of the 2722 sequences defined in the specification. A

CC polynucleotide of the invention may have a use in gene therapy. The human
 CC diagnostic and therapeutic polynucleotides (dithp) or polypeptides may be
 CC used to diagnose a particular condition, disease or disorder associated
 CC with human molecules, e.g. cell proliferative disorders,
 CC autoimmune/inflammatory disorders, developmental disorder, endocrine
 CC disorder, neurological disorders, gastrointestinal disorders, or
 CC infections caused by virus, bacteria, fungi or parasite. The dithp
 CC molecules may also be used in genetic mapping, in identifying individuals
 CC from minute biological samples, in detecting single nucleotide
 CC polymorphisms, as molecular weight markers, and for somatic or germline
 CC gene therapy. The present sequence represents a dithp protein of the
 CC invention. Note: The sequence data for this patent is not represented in
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at www.wipo.int/pct/en/sequences/listing.htm
 XX
 XX Sequence 214 AA;
 SQ
 Query Match 100.0%; Score 35; DB 8; Length 214;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DVSKRPS 7
 |||||
 DB 71 DVSKRPS 77
 Search completed: October 14, 2005, 16:12:42
 Job time : 54.8125 secs

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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:02:59 ; Search time 9.73438 Seconds
(without alignments)
69.190 Million cell updates/sec

Title: US-10-614-959-14
Perfect score: 35
Sequence: 1 DVSKRPS 7
Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	99	2	IG lambda chain -
2	34	97.1	646	2	probable receptor-
3	32	91.4	60	2	IG lambda chain V-
4	32	91.4	103	2	AL type amyloid fi
5	32	91.4	111	1	IG lambda chain V-
6	32	91.4	423	2	type IIS restricti
7	31	88.6	110	2	antibody light cha
8	31	88.6	111	1	IG lambda chain V-
9	31	88.6	111	2	IG lambda chain V
10	30	85.7	112	2	IG lambda chain V
11	30	85.7	112	2	IG lambda chain V-
12	30	85.7	416	2	type II site-speci
13	29	82.9	74	2	hypothetical prote
14	29	82.9	88	2	hypothetical prote
15	29	82.9	337	1	conserved hypotet
16	29	82.9	377	2	homeobox protein M
17	29	82.9	404	2	probable protein p
18	29	82.9	685	2	hypothetical prote
19	29	82.9	690	2	hypothetical prote
20	29	82.9	735	2	probable receptor-
21	29	82.9	972	2	hypothetical prote
22	29	82.9	1033	2	actin-interacting
23	29	82.9	1077	2	hypothetical prote
24	29	82.9	1245	2	hypothetical prote
25	28	80.0	91	2	ADP ATP carrier pr
26	28	80.0	111	1	IG lambda chain V-
27	28	80.0	189	2	GTP cyclohydrolase
28	28	80.0	189	2	GTP cyclohydrolase
29	28	80.0	235	2	IG lambda chain -

30 28 80.0 235 2 S14675
31 28 80.0 259 2 T40075
32 28 80.0 292 2 A64624
33 28 80.0 296 2 D71891
34 28 80.0 300 2 A82017
35 28 80.0 301 2 A82017
36 28 80.0 301 2 A82017
37 28 80.0 310 2 B97777
38 28 80.0 310 2 D71703
39 28 80.0 348 2 G87604
40 28 80.0 440 2 S65358
41 28 80.0 447 2 S35481
42 28 80.0 452 2 T40769
43 28 80.0 458 1 Z2BPC2
44 28 80.0 463 2 F90422
45 28 80.0 498 1 HYBSPA

ALIGNMENTS

RESULT 1
S36057
IG lambda chain - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C:Accession: S36057
R:Williams, S.C.
submitted to the EMBL Data Library, April 1993
A:Reference number: S36046
A:Accession: S36057
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-99 <WIL>
A:Cross-references: EMBL:Z22198; NID:g312319; PIDN:CAA80208.1; PID:g312320
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:15-92/Domain: immunoglobulin homology <IMM>

Query Match 100.0%; Score 35; DB 2; Length 99;
Best Local Similarity 100.0%; Pred. No. 1.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 52 DVSKRPS 58

RESULT 2
G85056
probable receptor-like protein kinase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Aug-2004
C:Accession: G85056
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: G85056
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-646 <STO>
A:Cross-references: UNIPROT:Q9XEC7; GB:NC_001268; NID:g7267207; PIDN:CAB77918.1; GSPDB:G

Query Match 97.1%; Score 34; DB 2; Length 646;
Best Local Similarity 85.7%; Pred. No. 12;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7

Db 606 DISKRPS 612
|:|||||

RESULT 3

A24626
Ig lambda chain V-II region (Har) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 25-Oct-1987 #sequence_revision 25-Oct-1987 #text_change 16-Aug-1996
C:Accession: A24626
R;Eulitz, M.; Linke, R.
Biochem. Biophys. Res. Commun. 366, 907-915, 1985
A:Title: Amyloid fibrils derived from V-region fragments from a 1
A:Reference number: A24626; PMID:86077295; PMID:3935132
A:Accession: A24626
A:Molecule type: protein
A:Residues: 1-60 <EUL>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 91.4%; Score 32; DB 2; Length 60;
Best Local Similarity 85.7%; Pred. No. 3.1;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7

Db 45 DVNKRPS 51
|:|||||

RESULT 4

A38923
AL type amyloid fibril protein precursor - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 21-Jan-2000
C:Accession: A38923
R;Eulitz, M.; Linke, R.P.
Biochem. Biophys. Res. Commun. 194, 1427-1434, 1993
A:Title: The precursor molecule of a V-lambda II-immunoglobulin light chain-derived amyloid
A:Reference number: A38923; PMID:93356823; PMID:8352801
A:Accession: A38923

A:Molecule type: protein
A:Residues: 1-95;96-103 <EUL>
C:Comment: This protein is derived from an immunoglobulin light chain of lambda type.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: amyloid; immunoglobulin
F;1-58/Product: AL type amyloid fibril protein #status predicted <MAT>
F;7-83/Domain: immunoglobulin homology <IMM>

Query Match 91.4%; Score 32; DB 2; Length 103;
Best Local Similarity 85.7%; Pred. No. 5.4;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7

Db 43 DVNKRPS 49
|:|||||

RESULT 5

L2HUTR
Ig lambda chain V-II region (Tro) - human (tentative sequence)
C:Species: Homo sapiens (man)
C:Date: 29-Jul-1981 #sequence_revision 29-Jul-1981 #text_change 09-Jul-2004
C:Accession: A01973
R;Scholz, R.; Yang, C.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 360, 1903-1918, 1979
A:Title: Zur Strukturregel der Antikörper. Die Primärstruktur eines monoklonalen IgA 1
A:Reference number: A01973; PMID:80114123; PMID:118915
A:Accession: A01973
A:Molecule type: protein
A:Residues: 1-111 <SCH>
A:Cross-references: UNIPROT:P01707
C:Comment: This chain was isolated from a myeloma protein.
C:Genetics:

A:Gene: GDB:IGLV@
A:Cross-references: GDB:119342; OMIM:147240
A:Map position: 22q11.2-22q11.2
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (lambda) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into larger superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: blocked amino end; heterotetramer; immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>
F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #status predicted
F;22-90/disulfide bonds: #status predicted

Query Match 91.4%; Score 32; DB 1; Length 111;
Best Local Similarity 85.7%; Pred. No. 5.9;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7

Db 52 DVTKRPS 58
|:|||||

RESULT 6

F64690
Type IIS restriction enzyme R protein - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: F64690
R;Tomb, J.F.; White, O.; Kerlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliak, H.G.; Glodek, A.; McKenn
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; PMID:97394467; PMID:9252185
A:Accession: F64690
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-423 <TOM>
A:Cross-references: UNIPROT:O25919; GB:AE000637; GB:AE000511; NID:g2314536; PIDN:AAD0841

Query Match 91.4%; Score 32; DB 2; Length 423;
Best Local Similarity 85.7%; Pred. No. 23;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7

Db 71 DMSKRPS 77
|:|||||

RESULT 7

S51149
antibody light chain V region - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 21-Jan-2000
C:Accession: S51149
R;de Kruijf, J.; Boel, E.; Logtenberg, T.
submitted to the EMBL Data Library, January 1995
A:Description: Selection and application of human SCFV antibody fragments from a semi-sy
A:Reference number: S51147
A:Accession: S51149
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-110 <DEK>
A:Cross-references: EMBL:X83712
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F;13-90/Domain: immunoglobulin homology <IMM>

Query Match 88.6%; Score 31; DB 2; Length 110;
Best Local Similarity 85.7%; Pred. No. 9.8;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7

Db 50 EVSKRPS 56
|:|||||

```

submitted to the EMBL Data Library, January 1993
A;Description: V-lambda-2 gene sequence of a high affinity anti-idiotypic IgM antibody
A;Reference number: S31515
A;Accession: S31515
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-112 <VAN>
A;Cross-references: EMBL:Z19546; NID:G33754; PIDN:CAA79606.1; PID:G33755
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>

Query Match      85.7%; Score 30; DB 2; Length 112;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
    |||||
Db 52 DVSNRPS 58

RESULT 11
S44105
Ig lambda chain V-J region - human
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-May-2001
C;Accession: S44105
R;Hawkins, R.E.; Zhu, D.; Ovecka, M.; Winter, G.; Hamblin, T.J.; Stevenson, F.K.
submitted to the EMBL Data Library, March 1994
A;Description: Idiotypic vaccination against human B-cell lymphoma: rescue of variable r
A;Reference number: S44105
A;Accession: S44105
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-112 <HAW>
A;Cross-references: EMBL:Z31388; NID:G472959; PIDN:CAA83263.1; PID:G940517
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>

Query Match      85.7%; Score 30; DB 2; Length 112;
Best Local Similarity 85.7%; Pred. No. 17;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
    |||||
Db 52 DVSNRPS 58

RESULT 12
S26836
type II site-specific deoxyribonuclease (EC 3.1.21.4) MboII - Moraxella bovis
C;Species: Moraxella bovis
C;Date: 03-Mar-1994 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C;Accession: S26836
R;Bocklage, H.; Heeger, K.; Mueller-Hill, B.
Nucleic Acids Res. 19, 1007-1013, 1991
A;Title: Cloning and characterization of the MboII restriction-modification system.
A;Reference number: S26835; MUID:91212177; PMID:2020540
A;Accession: S26836
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-416 <BOC>
A;Cross-references: UNIPROT:P23191; EMBL:X56977; NID:G44180; PIDN:CAA40298.1; PID:G44182
C;Keywords: hydrolase

Query Match      85.7%; Score 30; DB 2; Length 416;
Best Local Similarity 83.3%; Pred. No. 64;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRP 6
    |||||
Db 66 DISKRP 71

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RESULT 8
L2HUWN
Ig lambda chain V-II region (Win) - human (tentative sequence)
C;Species: Homo sapiens (man)
C;Date: 30-Nov-1979 #sequence_revision 30-Nov-1979 #text_change 09-Jul-2004
C;Accession: A01978
R;Chen, B.L.; Chiu, Y.Y.H.; Humphrey, R.L.; Poljak, R.J.
Biochim. Biophys. Acta 537, 9-21, 1978
A;Title: Amino acid sequence of the human myeloma lambda chain Win.
A;Reference number: A01978; MUID:79062503; PMID:102365
A;Accession: A01978
A;Molecule type: protein
A;Residues: 1-111 <CHE>
A;Cross-references: UNIPROT:P01712
C;Comment: This is a Bence Jones protein.
C;Genetics:
A;Gene: GDB:IGLV@
A;Cross-references: GDB:119342; OMIM:147240
A;Map position: 22q11.2-22q11.2
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: blocked amino end; heterotetramer
F;15-92/Domain: immunoglobulin homology <IMM>
F;1/Modified site: blocked amino end (Gln) (probably pyrrolidone carboxylic acid) #statu
F;22-90/Disulfide bonds: #status predicted

Query Match      88.6%; Score 31; DB 1; Length 111;
Best Local Similarity 85.7%; Pred. No. 9.9;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
    |||||
Db 52 DVDRKPS 58

RESULT 9
S36281
Ig lambda chain V region (clone alpha-FOG1-A3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 21-Jan-2000
C;Accession: S36281
R;Griffiths, A.D.; Malmqvist, M.; Marks, J.D.; Bye, J.M.; Embleton, M.J.; McCafferty, J.
EMBO J. 12, 725-734, 1993
A;Title: Human anti-self antibodies with high specificity from phage display libraries.
A;Reference number: S36256; MUID:93178448; PMID:7679990
A;Accession: S36281
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-111 <GRI>
A;Cross-references: EMBL:Z18823; NID:G33414; PIDN:CAA79275.1; PID:G939907
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-92/Domain: immunoglobulin homology <IMM>

Query Match      88.6%; Score 31; DB 2; Length 111;
Best Local Similarity 85.7%; Pred. No. 9.9;
Matches 6; Conservative 1; Mismatches 0; Indels -0; Gaps 0;

Qy 1 DVSKRPS 7
    |||||
Db 52 EVSKRPS 58

RESULT 10
S31515
Ig lambda chain V region - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000
C;Accession: S31515
R;van der Heijden, R.W.J.; Dytdehaag, F.G.C.M.; Osterhaus, A.D.M.E.

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RESULT 13

AH2642
 hypothetical protein Atu0540 [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C:Species: Agrobacterium tumefaciens
 C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
 C:Accession: AH2642
 R:Wood, D.W.; Secubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.
 erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
 ; Karp, P.; Romero, P.; Zhang, S.
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
 star, E.W.
 A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: AB2577; MUID:21608550; PMID:11743193
 A:Accession: AH2642
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-74 <KUR>
 A:Cross-references: UNIPROT:Q8UHW8; GB:AE008688; PIDN:AAL41558.1; PID:gl7738891; GSPDB:C
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: Atu0540
 A:Map position: circular chromosome

Query Match 82.9%; Score 29; DB 2; Length 74;
 Best Local Similarity 71.4%; Pred. No. 19;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
 |:|||||
 Db 2 DISKEPS 8

RESULT 14

A97425
 hypothetical protein AGR_C_956 [imported] - Agrobacterium tumefaciens (strain C58, Cere
 C:Species: Agrobacterium tumefaciens
 C:Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C:Accession: A97425
 R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman,
 A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.;
 Science 294, 2323-2328, 2001
 A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tum
 A:Reference number: A97359; MUID:21608551; PMID:11743194
 A:Accession: A97425
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-88 <KUR>
 A:Cross-references: UNIPROT:Q8UHW8; GB:AE007869; PIDN:AAK86354.1; PID:gl5155478; GSPDB:C
 C:Genetics:
 A:Gene: AGR_C_956
 A:Map position: circular chromosome

Query Match 82.9%; Score 29; DB 2; Length 88;
 Best Local Similarity 71.4%; Pred. No. 23;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
 |:|||||
 Db 16 DISKEPS 22

RESULT 15

E70191
 conserved hypothetical protein BB0734 - Lyme disease spirochete
 C:Species: Borrelia burgdorferi (Lyme disease spirochete)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: E70191
 R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White
 son, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
 ; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 390, 580-586, 1997
 A:Authors: Smith, H.O.; Venter, J.C.
 A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.
 A:Reference number: A70100; MUID:98065943; PMID:9403685
 A:Accession: E70191
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-337 <KLE>
 A:Cross-references: UNIPROT:O51676; GB:AE001173; GB:AE000783; NID:g2688665; PIDN:AAC6701
 A:Experimental source: strain B31
 C:Superfamily: translation factor, SUAS type

Query Match 82.9%; Score 29; DB 1; Length 337;
 Best Local Similarity 71.4%; Pred. No. 88;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
 |:|||||
 Db 141 MISKEPS 147

Search completed: October 14, 2005, 16:23:40
 Job time : 11.7344 secs

GenCore version 5.1.6
 Copyright (c) 1993 - 2005 Compugen Ltd.
 OM protein - protein search, using sw model
 Run on: October 14, 2005, 15:51:44 ; Search time 46.5938 seconds
 (without alignments)
 76.932 Million cell updates/sec

Title: us-10-614-959-14
 Perfect score: 35
 Sequence: 1 DVSKRPS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trenbl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	34	97.1	646	Q9XEC7	Q9xec7 arabidopsis
2	32	91.4	111	LV2D HUMAN	P01707 homo sapien
3	32	91.4	236	Q6PIQ7	Q6piq7 homo sapien
4	32	91.4	423	O25919	O25919 helicobacte
5	31	88.6	111	LV2I HUMAN	P01712 homo sapien
6	31	88.6	130	Q7MUS6	Q7mus6 porphyromon
7	31	88.6	233	Q7S4H3	Q7s4h3 neurospora
8	31	88.6	400	Q7S2L9	Q7s2l9 brachydanio
9	31	88.6	402	Q64WE5	Q64we5 bacteroides
10	31	88.6	486	O828G3	O828g3 streptomyce
11	31	88.6	728	Q7SF90	Q7sf90 neurospora
12	31	88.6	1292	Q6SLD6	Q6sl6 cochliobolu
13	31	88.6	1766	Q7SE06	Q7se06 ashbya goss
14	31	88.6	1935	Q7S9 HUMAN	Q7s924 ashbya goss
15	30	85.7	164	BFR1 MAGMG	O50171 magnetospir
16	30	85.7	212	Q9V6F8	Q9v6f8 drosophila
17	30	85.7	233	Q6PIA3	Q6pia3 homo sapien
18	30	85.7	236	Q6PFS3	Q6pfs3 homo sapien
19	30	85.7	267	Q9ETM2	Q9etm2 homo sapien
20	30	85.7	279	Y170 BUCBP	Q89as2 buchnera ap
21	30	85.7	283	Q70914	Q70914 prunus necr
22	30	85.7	283	Q70918	Q70918 prunus necr
23	30	85.7	285	Q70142	Q70142 prunus necr
24	30	85.7	327	Q86V04	Q86v04 homo sapien
25	30	85.7	378	Q9XY82	Q9xy82 enchytraeus
26	30	85.7	385	Q7S098	Q7s098 neurospora
27	30	85.7	401	Q6DXH1	Q6dxx1 homo sapien
28	30	85.7	416	T2M2 MORBO	P23191 moraxella b
29	30	85.7	508	Q80U48	Q80u48 mus musculu
30	30	85.7	530	Q6PHC0	Q6phc0 mus musculu
31	30	85.7	654	Q8CAA2	Q8caa2 mus musculu

32	30	85.7	674	2	Q9DBJ2	Q9dbj2 mus musculu
33	30	85.7	706	1	TM24 MOUSE	..O14523 homo sapien
34	30	85.7	706	1	TM24 MOUSE	Q80x80 mus musculu
35	30	85.7	747	2	Q6DOL7	Q6dol7 erwinia car
36	30	85.7	833	2	Q6ADP4	Q6adp4 leifsonia x
37	30	85.7	1036	2	Q6LMQ4	Q6lmq4 methanococc
38	30	85.7	1059	2	Q84QQ1	Q84qq1 bacteroides
39	30	85.7	1372	2	Q8SX99	Q8sx99 drosophila
40	30	85.7	1372	2	Q9VN46	Q9vn46 drosophila
41	29	82.9	59	2	Q6YEV3	Q6yev3 vitis vinif
42	29	82.9	74	2	Q8UHW8	Q8uhw8 agrobacteri
43	29	82.9	80	2	Q6LK05	Q6lk05 photobacter
44	29	82.9	88	2	Q7D190	Q7d190 agrobacteri
45	29	82.9	103	2	Q6D0T2	Q6d0t2 erwinia car

ALIGNMENTS

RESULT 1
 Q9XEC7 ID Q9XEC7 PRELIMINARY; PRT; 646 AA.
 AC Q9XEC7;
 DT 01-NOV-1999 (TRENBLrel. 12, Created)
 DT 01-NOV-1999 (TRENBLrel. 12, Last sequence update)
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)
 DE Putative receptor-like protein kinase.
 GN Name=t26N6.11; Synonyms=AT4G04500;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zhong J., Ma P., Parnell L.D., Chen C.-N., Chen E.Y.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Parnell L.D.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Zhong J., Ma P., Parnell L.D., Chen C.N., Chen E.Y., Mewes H.W.,
 RL Lemcke K., Mayer K.F.X.;
 RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- SIMILARITY: Belongs to the Ser/Thr protein kinase family.
 DR EMBL; AF076243; AAD29762.1; -.
 DR EMBL; AL161500; CAB77918.1; -.
 DR PIR; G85056; G85056.
 DR HSRP; P06239; 3LCK.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0016740; F:transferase activity; IEA.
 DR GO; GO:0006458; P:protein amino acid phosphorylation; IEA.
 DR InterPro; IPR002902; DUF26.
 DR InterPro; IPR011009; Kinase like.
 DR InterPro; IPR000719; Prot kinase.
 DR InterPro; IPR008271; Ser_thr_pkin_AS.
 DR Pfam; PF01657; DUF26; 2.
 DR Pfam; PF00069; Pkinase; 1.
 DR ProDom; PD000001; Prot_kinase; 1.
 DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
 DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
 DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
 DR ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
 KW Transference.
 SQ SEQUENCE 646 AA; 73439 MW; E1200574D5864207 CRC64;

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Query Match          97.1%; Score 34; DB 2; Length 646;
Best Local Similarity 85.7%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 606 DISKRPS 612

RESULT 2
LV2D HUMAN STANDARD; PRT; 111 AA.
AC P01707:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-II region TR0.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=80114123; PubMed=118915;
RA Scholz R., Yang C., Hilschmann N.;
RT "Rule of antibody structure. Primary structure of a human monoclonal
RT IgA1-immunoglobulin (myeloma protein Tr0). VI. Amino acid sequence of
RT the L-chain, lambda-type, subgroup II."
RL Hoppe-Sejler's Z. Physiol. Chem. 360:1903-1918(1979).
CC -!- MISCELLANEOUS: This chain was isolated from a myeloma protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01973; L2HUTR.
DR HSSP; P01709; 2MCG.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00447; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
KW Pyridolone carboxylic acid.
FT DOMAIN 1 106 Ig-like.
FT MOD_RES 1 1 Pyridolone carboxylic acid.
FT DISULFID 22 90 By similarity.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11561 MW; 99DC457A12E8F6E1 CRC64;

Query Match          91.4%; Score 32; DB 1; Length 111;
Best Local Similarity 85.7%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 52 DVTKRPS 58

RESULT 3
Q6PIQ7 PRELIMINARY; PRT; 236 AA.
AC Q6PIQ7:
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

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TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmitt J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalitus J., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC030983; AAH30983.1; -.
DR HSSP; P01709; 1A8U.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF07654; CI-set; 1.
DR SMART; SM00409; IG; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25021 MW; 4A07BEF60A5FD465 CRC64;

Query Match          91.4%; Score 32; DB 2; Length 236;
Best Local Similarity 85.7%; Pred. No. 69;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 71 DVNKRPS 77

RESULT 4
O25919 PRELIMINARY; PRT; 423 AA.
AC O25919:
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Type IIS restriction enzyme R protein (MBOIIR).
GN OrderedLocustNames=HP1366;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=97394467; PubMed=9252185; DOI=10.1038/41483;
RA Tomb J.-P., White O., Kervatage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R., Kirkness E.F.,
RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Khalak H.G.,
RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J.,

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RA Glodek A., McKenney K., FitzGerald L.M., Lee N., Adams M.D.,
RA Hickey E.K., Berg D.E., Gocayne J.D., Uterback T.R., Peterson J.D.,
RA Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,
RA Watthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
RA Smith H.O., Fraser C.M., Venter J.C.,
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori.", 388:539-547(1997).
RL Nature 388:539-547(1997).
DR EMBL; AE000637; AAD08410.1; -.
DR PIR; F64690; F64690.
DR TIGR; HP1366; -.
DR InterPro; IPR003615; HNH_nuc.
DR SMART; SM00507; HNHc; 1.
DR Complete proteome.
SQ SEQUENCE 423 AA; 50047 MW; 9086E51C9FE4B58E CRC64;

Query Match 91.4%; Score 32; DB 2; Length 423;
Best Local Similarity 85.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKEPS 7
Db 71 DMSKEPS 77

RESULT 5
LV21 HUMAN
ID LV21 HUMAN STANDARD; PRT; 111 AA.
AC P01712;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-II region WIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=79062503; PubMed=102365; DOI=10.1016/0005-2795(78)90598-6;
RA Chen B.L., Chiu Y.-Y.H., Humphrey R.L., Poljak R.J.;
RT "Amino acid sequence of the human myeloma lambda chain Win. ";
RL Biochim. Biophys. Acta 537:9-21(1978).
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A01978; L2HWN.
DR HSP; P01709; 1DCI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Bence-Jones protein; Direct protein sequencing;
KW Immunoglobulin V region; Pyridone carboxylic acid.
FT DOMAIN 1 106
FT MOD_RES 1 1 Pyridone carboxylic acid.
FT DISULFID 22 90 By similarity.
FT NON_TER 111 111
SQ SEQUENCE 111 AA; 11694 MW; 8C3CE95FE721B87C CRC64;

Query Match 88.6%; Score 31; DB 1; Length 111;
Best Local Similarity 85.7%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKEPS 7
Db 52 DVSKEPS 58

RESULT 6

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Q7MUS6
ID Q7MUS6 PRELIMINARY; PRT; 130 AA.
AC Q7MUS6;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN OrderedlocusNames=PGI409;
OS Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteria; Bacteroidetes; Bacteroides (Class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=W83;
RX MEDLINE=22829867; PubMed=12949112;
RX DOI=10.1128/JB.185.18.5591-5601.2003;
RA Nelson K.E., Fleischmann R.D., DeBoy R.T., Paulsen I.T., Fouts D.E.,
RA Eisen J.A., Daugherty S.C., Dodson R.J., Durkin A.S., Gwinn M.L.,
RA Hatt D.H., Kolonay J.F., Nelson W.C., Mason T.M., Tallon L., Gray J.,
RA Granger D., Tettelin H., Dong H., Galvin J.L., Duncan M.J.,
RA Dewhirst F.E., Fraser C.M.;
RT "Complete genome sequence of the oral pathogenic bacterium
RT Porphyromonas gingivalis strain W83.";
RL J. Bacteriol. 185:5591-5601(2003).
DR EMBL; AE017176; AAQ66466.1; -.
DR TIGR; PG1409; -.
DR Complete proteome; Hypothetical protein.
KW SEQUENCE 130 AA; 14455 MW; 3F2E1F64F23B5805 CRC64;

Query Match 88.6%; Score 31; DB 2; Length 130;
Best Local Similarity 71.4%; Pred. No. 63;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKEPS 7
Db 107 DISRPS 113

RESULT 7
Q7S4H3
ID Q7S4H3 PRELIMINARY; PRT; 233 AA.
AC Q7S4H3;
DT 01-MAR-2004 (TRENBLrel. 26, Created)
DT 01-MAR-2004 (TRENBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Hypothetical protein.
GN Name=NCU02220.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehm B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamysseilis M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Krystofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA DeSouza C.C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbold D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

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CC      preliminary data.
DR      EMBL; AABX01000366; EAA30397.1; -.
DR      GO; GO:0030288; C:periplasmic space (sensu Gram-negative Bact. . .; IEA.
DR      GO; GO:0015035; F:protein disulfide oxidoreductase activity; IEA.
DR      InterPro; IPR001853; DSBa.
DR      InterPro; IPR010986; Dsba_insertion.
DR      Pfam; PF01323; DSBa; 1.
KW      Hypothetical protein.
SQ      SEQUENCE 233 AA; 25367 MW; 50B8F4A369168929 CRC64;

Query Match      88.6%; Score 31; DB 2; Length 233;
Best Local Similarity 85.7%; Pred. No. 1.2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 DVSKRPS 7
Db      222 DVSERPS 228

RESULT 8
ID      Q7SZL9      PRELIMINARY;      PRT;      400 AA.
AC      Q7SZL9;
DT      01-OCT-2003 (TrEMBLrel. 25, Created)
DT      01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      ATP-gated ionotropic P2X receptor subunit 2.
GN      Name=p2rx2; Synonyms=p2xr2;
OS      Brachydanio rerio (Zebrafish) (Danio rerio).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC      Cyprinidae; Danio.
OX      NCBI_TaxID=7955;
RN      [1]
SEQUENCE FROM N.A.
RX      MEDLINE=22943235; PubMed=14580944; DOI=10.1016/S0306-4522(03)00566-9;
RA      Kucenas S., Li Z., Cox J.A., Egan T.M., Voigt M.M.;
RT      "Molecular characterization of the zebrafish P2X receptor subunit gene
      family";
RL      Neuroscience 121:935-945(2003).
DR      EMBL; AY292650; AAO21195.1; -.
DR      ZFIN; ZDB-GENE-030319-2; p2rx2.
DR      GO; GO:0009503; C:light-harvesting complex (sensu Viridiplantae); IEA.
DR      GO; GO:0016020; C:membrane; IEA.
DR      GO; GO:0005524; F:ATP binding; IEA.
DR      GO; GO:0005216; F:ion channel activity; IEA.
DR      GO; GO:0016978; F:lipote-protein ligase B activity; IEA.
DR      GO; GO:0004872; F:receptor activity; IEA.
DR      GO; GO:0006091; P:energy pathways; IEA.
DR      GO; GO:0006811; P:ion transport; IEA.
DR      InterPro; IPR000066; Antenna_a/b.
DR      InterPro; IPR001429; P2X_receptor.
DR      Pfam; PF00864; P2X_receptor; 1.
DR      TIGRFAMs; TIGR00863; P2X; 1.
KW      Receptor.
SQ      SEQUENCE 400 AA; 45752 MW; EE571C00171609F5 CRC64;

Query Match      88.6%; Score 31; DB 2; Length 400;
Best Local Similarity 85.7%; Pred. No. 2e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 DVSKRPS 7
Db      369 DVSKQPS 375

RESULT 9
ID      Q64WE5      PRELIMINARY;      PRT;      402 AA.
AC      Q64WE5;
DT      25-OCT-2004 (TrEMBLrel. 28, Created)
DT      25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT      25-OCT-2004 (TrEMBLrel. 28, Last annotation update)

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DE      Predicted nucleoside-diphosphate sugar epimerase.
DR      ORFNames=BF1430;
OS      Bacteroides fragilis.
OC      Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC      Bacteroidaceae; Bacteroides.
OX      NCBI_TaxID=817;
RN      [1]
SEQUENCE FROM N.A.
RC      STRAIN=YCH46;
RA      Kuwahara T., Yamashita A., Hirakawa H., Nakayama H., Toh H., Okada N.,
RA      Kuwaha S., Hattori M., Hayashi T., Ohnishi Y.;
RT      "Genomic analysis of Bacteroides fragilis reveals extensive DNA
      RT      inversions regulating cell surface adaptation.";
RL      Proc. Natl. Acad. Sci. U.S.A. 0:0-0(2004).
DR      EMBL; AP006841; BAD48181.1; -.
SQ      SEQUENCE 402 AA; 45596 MW; 2D56A6DAF87797CC CRC64;

Query Match      88.6%; Score 31; DB 2; Length 402;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DVSKRP 6
Db      348 DVSKRP 353

RESULT 10
ID      Q828G3      PRELIMINARY;      PRT;      486 AA.
AC      Q828G3;
DT      01-JUN-2003 (TrEMBLrel. 24, Created)
DT      01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT      01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE      Putative cytochrome P450.
GN      Name=cyp24; OrderedLocustNames=SAV6706;
OS      Streptomyces avermitilis.
OC      Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC      Streptomycineae; Streptomycetaceae; Streptomyces.
OX      NCBI_TaxID=33903;
RN      [1]
SEQUENCE FROM N.A.
RC      STRAIN=MA-4680;
RX      MEDLINE=21477403; PubMed=11572948; DOI=10.1073/pnas.211433198;
RA      Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,
RA      Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,
RA      Kikuchi H., Shiba T., Sakaki Y., Hattori M.;
RT      "Genome sequence of an industrial microorganism Streptomyces
      RT      avermitilis: deducing the ability of producing secondary
      RT      metabolites.";
RL      Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).
RN      [2]
SEQUENCE FROM N.A.
RC      STRAIN=MA-4680;
RX      MEDLINE=22608306; PubMed=12692562;
RA      Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,
RA      Sakaki Y., Hattori M., Omura S.;
RT      "Complete genome sequence and comparative analysis of the industrial
      RT      microorganism Streptomyces avermitilis.";
RL      Biotechnol. 21:526-531(2003).
CC      -!- SIMILARITY: Belongs to the cytochrome P450 family.
DR      EMBL; AP005047; BAC74417.1; -.
DR      HSSP; 09L142; 1GWI.
DR      GO; GO:0004497; F:monooxygenase activity; IEA.
DR      GO; GO:0006118; P:electron transport; IEA.
DR      InterPro; IPR002397; BP450.
DR      InterPro; IPR001128; Cytochrome_P450.
DR      PRINTS; PR00359; BP450.
DR      PROSITE; PS00086; CYTOCHROME_P450; UNKNOWN 1.
KW      Complete proteome; Heme; Monooxygenase; Oxidoreductase.
SQ      SEQUENCE 486 AA; 53354 MW; A728B74F6592E265 CRC64;

Query Match      88.6%; Score 31; DB 2; Length 486;
Best Local Similarity 85.7%; Pred. No. 2.5e+02;

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Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|||||
Db 428 DVSKRPS 434

RESULT 11

ID Q7SF90 PRELIMINARY; PRT; 728 AA.
AC Q7SF90; 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU00559.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun B.L., Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D., Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S., Kanai M., Kamysellis M., Mauceli E., Bielek C., Rudd S., Frishman D., Krystofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S., Cogoni C., Macino G., Catcheside D., Li W., Pratt R.J., Osmani S.A., DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R., Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R., Natvig D.O., Alex L.A., Mannhaupt G., Ebbel D.J., Freitag M., Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa.";
RL Nature 0:0-0(2003).
CC -!- CAUTION: The sequence shown here is derived from an EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is preliminary data.
CC EMBL; AABX01000022; EAA35484.1; -.
SQ SEQUENCE 728 AA; 79550 MW; 05A688EBD3850B79 CRC64;

Query Match 88.6%; Score 31; DB 2; Length 728;
Best Local Similarity 85.7%; Pred. No. 3.8e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|||||
Db 336 DASKRPS 342

RESULT 12

ID Q6SLD6 PRELIMINARY; PRT; 1292 AA.
AC Q6SLD6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Putative histidine kinase HHK1lp.
GN Name=HHK1;
OS Cochliobolus heterostrophus (Drechslera maydis).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Dothideomycetes;
OC Pleosporales; Pleosporaceae; Cochliobolus.
OX NCBI_TaxID=5016;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C4;
RX PubMed=14665450; DOI=10.1128/EC.2.6.1151-1161.2003;
RA Catlett N.L., Yoder O.C., Turgon B.G.;
RT "Whole-genome analysis of two-component signal transduction genes in

RT fungal pathogens.";
RL Eukaryotic Cell 2:1151-1161(2003).
CC -!- SIMILARITY: Contains 1 histidine kinase domain.
EMBL; AY456014; AAR29890.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0003677; F:DNA binding; IEA.
DR GO; GO:0016301; F:kinase activity; IEA.
DR GO; GO:0000156; F:two-component sensor molecule activity; IEA.
DR GO; GO:0000155; F:two-component sensor molecule activity; IEA.
DR GO; GO:0007600; P:sensory perception; IEA.
DR GO; GO:0000160; P:two-component signal transduction system (p...); IEA.
DR InterPro; IPR003594; AtPbind_Arpase.
DR InterPro; IPR004358; Bact_sens_pr_C.
DR InterPro; IPR011006; Chey_like.
DR InterPro; IPR005467; His_kinase.
DR InterPro; IPR003661; His_kinA_N.
DR InterPro; IPR001789; Response_reg.
DR Pfam; PF02518; HAIPase_c; 1.
DR Pfam; PF00512; HSKA; 1.
DR PRINTS; PR00072; Response_reg; 1.
DR PRINTS; PR00344; BCTRLSENSOR.
DR ProDom; PD000039; Response_reg; 1.
DR SMART; SM00387; HAIPase_c; 1.
DR SMART; SM00388; HSKA; 1.
DR SMART; SM00448; REC; 1.
DR PROSITE; PS010109; HIS_KIN; 1.
DR PROSITE; PS01110; RESPONSE_REGULATORY; 1.
KW Kinase; Phosphorylation; Sensory transduction.
SQ SEQUENCE 1292 AA; 14730 MW; 57010F00609FF49B CRC64;

Query Match 88.6%; Score 31; DB 2; Length 1292;
Best Local Similarity 85.7%; Pred. No. 6.9e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|||||
Db 45 DVDKRPS 51

RESULT 13

Q75E06
ID Q75E06 PRELIMINARY; PRT; 1766 AA.
AC Q75E06;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE ABL133Cp.
GN ORFNames=ABL133C;
OS Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX NCBI_TaxID=33169;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10895;
RA Voegeli S.E., Dietrich F.S., Brachat S., Lerch A., Gaffney T., Philippsen P.;
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016815; AAS0638.1; -.
DR AGP; ABL133C; -.
SQ SEQUENCE 1766 AA; 179132 MW; BEC73A1CF69F2EA3 CRC64;

Query Match 88.6%; Score 31; DB 2; Length 1766;
Best Local Similarity 85.7%; Pred. No. 9.6e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
|||||
Db 1445 DVSRPS 1451

RESULT 14

AT99_HUMAN
 ID AT99_HUMAN STANDARD; PRT; 1935 AA.
 AC Q9P2N4; Q9NR29;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE ADAMTS-9 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase
 DE with thrombospondin motifs 9) (ADAM-TS 9) (ADAM-TS9).
 GN Name=ADAMTS9; Synonyms=KIAA1312;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 3).
 RC TISSUE=Fetal;
 RX MEDLINE=20396138; PubMed=10936055; DOI=10.1006/geno.2000.6246;
 RA Clark M.E., Kelnar G.S., Turbeville L.A., Boyer A., Arden K.A.,
 RA Maki R.A.;
 RT "ADAMTS 9, a novel member of the ADAM-TS/Metallospandin gene family.";
 RL Genomics 67:343-350(2000).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND FUNCTION.
 RX MEDLINE=22513925; PubMed=12514189; DOI=10.1074/jbc.M211009200;
 RA Somerville R.P., Longpre J.-M., Jungers K.A., Engle J.M., Ross M.,
 RA Evanko S., Wight T.N., Leduc R., Apte S.S.;
 RT "Characterization of ADAMTS-9 and ADAMTS-20 as a distinct ADAMTS
 RT subfamily related to Caenorhabditis elegans GON-1.";
 RL J. Biol. Chem. 278:9503-9513(2003).
 RN [3]
 RP SEQUENCE OF 159-1935 FROM N.A. (ISOFORM 2).
 RC TISSUE=Brain;
 RX MEDLINE=20181126; PubMed=10718198;
 RA Nagase T., Kikuno R., Ishikawa K.-I., Hirosewa M., Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XVI.
 RT The complete sequences of 150 new cDNA clones from brain which code
 RT for large proteins in vitro.";
 RL DNA Res. 7:65-73(2000).
 CC -1- FUNCTION: Cleaves the large aggregating proteoglycans, aggrecan
 CC and versican.
 CC -1- CATALYTIC ACTIVITY: Cleaves aggrecan at the 1818-Glu-|-Ala-1839
 CC site and versican at the 1428-Glu-|-Ala-1429 site.
 CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted. Associated with the extracellular
 CC matrix (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=3;
 CC Name=1; Synonyms=ADAMTS-9B;
 CC IsoId=Q9P2N4-3; Sequence=Displayed;
 CC Name=2; Synonyms=Long;
 CC IsoId=Q9P2N4-1; Sequence=VSP_007548, VSP_007549;
 CC Note=May result from the retention of an intron in the cDNA
 CC leading to a premature stop codon;
 CC Name=3; Synonyms=Short;
 CC IsoId=Q9P2N4-2; Sequence=VSP_005499, VSP_005500;
 CC -1- TISSUE SPECIFICITY: Highly expressed in all fetal tissues.
 CC Expressed in a number of adult tissues with highest expression in
 CC heart, placenta and skeletal muscle.
 CC -1- DOMAIN: The spacer domain and the TSP type-1 domains are important
 CC for a tight interaction with the extracellular matrix (By
 CC similarity).
 CC -1- DOMAIN: The ancillary domains, including the TSPs domain, are
 CC required for specific extracellular localization and for its
 CC versicanase and aggrecanase activities.
 CC -1- PTM: The precursor is cleaved by a furin endopeptidase (By
 CC similarity).
 CC -1- SIMILARITY: Belongs to the peptidase M12B family.
 CC -1- SIMILARITY: Contains 1 disintegrin-like domain.
 CC -1- SIMILARITY: Contains 1 GON domain.
 CC -1- SIMILARITY: Contains 15 TSP type-1 domains.
 CC -----
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 DR EMBL; AF261918; AAF89106.1; -;
 DR EMBL; AF488803; AAO15765.1; -;
 DR EMBL; AB037733; BAA92550.1; -;
 DR EMBL; P07996; ILSL.
 DR MEROPS; M12.021; -;
 DR Genew; HGNC:13202; ADAMTS9.
 DR MIM; 605421; -;
 DR GO; GO:0008237; F:metallopeptidase activity; TAS.
 DR GO; GO:0007275; P:development; TAS.
 DR GO; GO:0005516; P:glycoprotein catabolism; TAS.
 DR InterPro; IPR010294; ADAM_spacer1.
 DR InterPro; IPR001762; Disintegrin.
 DR InterPro; IPR001818; Pept_M10A_M12B.
 DR InterPro; IPR006025; Pept_M_Zn_BS.
 DR InterPro; IPR001590; Peptidase_M12B.
 DR InterPro; IPR002870; Peptidase_M12B_N.
 DR InterPro; IPR000884; TSP1.
 DR Pfam; PF05986; ADAM_spacer1; 1.
 DR Pfam; PF01562; Pep_M12B_propep; 1.
 DR Pfam; PF01421; Reprolysin; 1.
 DR Pfam; PF00090; TSP_1; 13.
 DR SMART; SM00209; TSP1; 15.
 DR PROSITE; PS00215; ADAM_MEPPO; 1.
 DR PROSITE; PS00546; CYSTEINE_SWITCH; FALSE_NEG.
 DR PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
 DR PROSITE; PS00214; DISINTEGRIN_2; FALSE_NEG.
 DR PROSITE; PS00092; TSP1; 14.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 KW Alternative splicing; Extracellular matrix; Glycoprotein; Hydrolase;
 KW Metalloprotease; Repeat; Signal; Zinc; Zymogen.
 FT SIGNAL 1 18 Potential.
 FT PROPEP 19 287
 FT CHAIN 288 1935 ADAMTS-9.
 FT DOMAIN 293 499 Metalloprotease.
 FT DOMAIN 509 587 Disintegrin-like.
 FT TSP type-1 1. TSP type-1 1.
 FT Cys-rich. Cys-rich.
 FT DOMAIN 753 877 Spacer.
 FT TSP type-1 2. TSP type-1 2.
 FT TSP type-1 3. TSP type-1 3.
 FT TSP type-1 4. TSP type-1 4.
 FT TSP type-1 5. TSP type-1 5.
 FT TSP type-1 6. TSP type-1 6.
 FT TSP type-1 7. TSP type-1 7.
 FT TSP type-1 8. TSP type-1 8.
 FT TSP type-1 9. TSP type-1 9.
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 FT TSP type-1 13. TSP type-1 13.
 FT TSP type-1 14. TSP type-1 14.
 FT TSP type-1 15. TSP type-1 15.
 FT GON. GON.
 FT Poly-Ser. Poly-Ser.
 FT Cysteine switch (Potential).
 FT Zinc (catalytic) (By similarity).
 FT ACT_SITE 435 435 By similarity.
 FT METAL 438 438 Zinc (catalytic) (By similarity).
 FT METAL 444 444 Zinc (catalytic) (By similarity).
 FT CARBOHYD 112 112 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 135 135 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 271 271 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 749 749 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 840 840 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1213 1213 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1267 1267 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 1788 1788 N-linked (GlcNAc...) (Potential).

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FT CAROHVD 1806 1806 N-linked (GlcNAc...) (Potential).
FT VARSPLIC 1064 1072 CLVTCGKH -> VWRVGCYFP (in isoform 3).
FT VARSPLIC 1073 1935 /FTId=VSP 005499.
FT VARSPLIC 1624 1629 /FTId=VSP 005500.
FT VARSPLIC 1624 1629 CSVTCG -> VPSWEL (in isoform 2).
FT VARSPLIC 1630 1935 /FTId=VSP 007548.
FT CONFLICT 46 46 /FTId=VSP 007549.
FT CONFLICT 96 96 S -> G (in Ref. 1).
FT CONFLICT 182 182 P -> S (in Ref. 1).
FT CONFLICT 367 367 D -> G (in Ref. 2).
FT CONFLICT 1117 1117 F -> L (in Ref. 1).
FT CONFLICT 1935 1935 V -> G (in Ref. 3).
SQ SEQUENCE 1935 AA; 216556 MW; FD3D51E88300A3C6 CRC64;

Query Match      88.6%; Score 31; DB 1; Length 1935;
Best Local Similarity 100.0%; Pred. No. 1.1e+03; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DVSKRP 6
Db      1596 DVSKRP 1601

RESULT 15
BFR1 MAGMG
ID BFR1 MAGMG STANDARD; PRT; 164 AA.
AC OS0171;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Bacterioferritin subunit 1 (BFR 1).
GN Name=bfr1;
OS Magnetospirillum magnetotacticum (Aquispirillum magnetotacticum).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
OC Rhodospirillaceae; Magnetospirillum.
OX NCBI_TaxID=188;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MS-1;
RX MEDLINE=98072426; PubMed=9409768; DOI=10.1016/S0378-1119(97)00424-1;
RA Bertani L.E., Huang J.S., Weir B.A., Kirschvink J.L.;
RT "Evidence for two types of subunits in the bacterioferritin of
RL Magnetospirillum magnetotacticum.";
RT Gene 201:31-36(1997).
CC -!- FUNCTION: May perform analogous functions in iron detoxification
CC and storage to that of animal ferritins (By similarity).
CC -!- COFACTOR: Binds 1 heme b (iron-protoporphyrin IX) group per
CC monomer (Potential).
CC -!- SUBUNIT: Oligomer of 24 identical subunits (By similarity).
CC -!- MISCELLANEOUS: The di-iron binding site functions as active site
CC where iron ions are oxidized from iron(II) to iron(III) before
CC they are stored (By similarity).
CC -!- SIMILARITY: Belongs to the bacterioferritin family.
CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF001959; AAC91253.1; --
CC HSP; F11056; 1BCF.
CC InterPro; IPR002024; Bacterioferritin.
CC InterPro; IPR009078; Ferritin/RR like.
CC InterPro; IPR008331; Ferritin Dps.
CC InterPro; IPR009040; Ferritin_like.
CC Pfam; PF00210; Ferritin; 1.
CC PRINTS; PR00601; BACFERRITIN.

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DR ProDom; P0002269; Bacterioferritin; 1.
DR TIGRFAMs; TIGR00754; bfr; 1.
DR PROSITE; PS00549; BACTERIOFERRITIN; 1.
DR PROSITE; PS09005; FERRITIN LIKE; 1.
KW Heme; Iron; Iron storage; Metal-binding.
FT DOMAIN 1 147 Ferritin-like diiron.
FT METAL 18 18 Iron 1 (By similarity).
FT METAL 49 49 Iron (heme axial ligand) (Potential).
FT METAL 51 51 Iron 1 (By similarity).
FT METAL 51 51 Iron 2 (By similarity).
FT METAL 54 54 Iron 1 (By similarity).
FT METAL 94 94 Iron 2 (By similarity).
FT METAL 129 129 Iron 1 (By similarity).
FT METAL 129 129 Iron 2 (By similarity).
FT METAL 132 132 Iron 2 (By similarity).
SQ SEQUENCE 164 AA; 18491 MW; 6B837DCAFC72358 CRC64;

Query Match      85.7%; Score 30; DB 1; Length 164;
Best Local Similarity 83.3%; Pred. No. 1.4e+02; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      1 DVSKRP 6
Db      70 DVSKRP 75

Search completed: October 14, 2005, 16:19:57
Job time : 48.5938 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:00:04 ; Search time 13.7812 Seconds
(without alignments)
37.917 Million cell updates/sec

Title: US-10-614-959-14
Perfect score: 35
Sequence: 1 DVSKRPS 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
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4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCUTS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	7	US-09-383-667-14	Sequence 14, Appl
2	35	100.0	111	US-08-652-816A-15	Sequence 15, Appl
3	35	100.0	112	US-09-025-769B-19	Sequence 19, Appl
4	35	100.0	112	US-09-490-070A-19	Sequence 19, Appl
5	35	100.0	112	US-09-490-153-19	Sequence 19, Appl
6	35	100.0	112	US-09-490-324-19	Sequence 19, Appl
7	31	88.6	7	US-09-383-667-25	Sequence 25, Appl
8	31	88.6	7	US-09-424-840B-125	Sequence 125, Appl
9	31	88.6	235	US-08-378-939-12	Sequence 12, Appl
10	31	88.6	236	US-08-487-550-10	Sequence 10, Appl
11	31	88.6	236	US-09-526-098-10	Sequence 10, Appl
12	31	88.6	236	US-09-383-916-10	Sequence 10, Appl
13	31	88.6	1039	US-09-949-016-7859	Sequence 7859, Ap
14	31	88.6	1882	US-09-369-364A-13	Sequence 13, Appl
15	30	85.7	110	US-09-025-769B-33	Sequence 33, Appl
16	30	85.7	110	US-09-025-769B-53	Sequence 53, Appl
17	30	85.7	110	US-09-490-070A-33	Sequence 33, Appl
18	30	85.7	110	US-09-490-070A-53	Sequence 53, Appl
19	30	85.7	110	US-09-490-153-33	Sequence 33, Appl
20	30	85.7	110	US-09-490-153-53	Sequence 53, Appl
21	30	85.7	110	US-09-490-324-33	Sequence 33, Appl
22	30	85.7	110	US-09-490-324-53	Sequence 53, Appl
23	29	82.9	215	US-09-247-373B-42	Sequence 42, Appl
24	28	80.0	111	US-09-212-290-17	Sequence 17, Appl
25	28	80.0	140	US-09-252-991A-23989	Sequence 23989, A
26	28	80.0	217	US-09-134-000C-5577	Sequence 5577, Ap
27	28	80.0	294	US-09-134-000C-4555	Sequence 4555, Ap

Sequence 43922, A
Sequence 18161, A
Sequence 2750, Ap
Sequence 15, Appl
Sequence 11, Appl
Sequence 423, App
Sequence 2, Appl
Sequence 15, App
Sequence 11, Appl
Sequence 17949, A
Sequence 33080, A
Sequence 53297, A
Sequence 476, App
Sequence 22912, A
Sequence 4891, Ap
Sequence 3333, Ap

ALIGNMENTS

RESULT 1
US-09-383-667-14
; Sequence 14, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Haas, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 14
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-14

Query Match 100.0%; Score 35; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 DVSKRPS 7
Db 1 DVSKRPS 7
|||||

RESULT 2
US-08-652-816A-15
; Sequence 15, Application US/08652816A
; Patent No. 5872215
; GENERAL INFORMATION:
; APPLICANT: Osbourn, JK
; APPLICANT: Allen, DJ
; APPLICANT: McCafferty, JG
; TITLE OF INVENTION: Specific binding members, materials and
; TITLE OF INVENTION: methods.
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,816A
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9125579.4
; FILING DATE: 02-DEC-1991
; APPLICATION NUMBER: GB 9125579.8
; FILING DATE: 02-DEC-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206372.6
; FILING DATE: 23-SEP-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9525004.9
; FILING DATE: 07-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9610824.6
; FILING DATE: 23-MAY-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/02240
; FILING DATE: 02-DEC-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/244,597
; FILING DATE: 01-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: David W. Clough
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/33308
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; US-08-652-816A-15

Query Match 100.0%; Score 35; DB 2; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 51 DVSKRPS 57

RESULT 3
US-09-025-769B-19
; Sequence 19, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas

; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-025-769B-19

Query Match 100.0%; Score 35; DB 3; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 52 DVSKRPS 58

RESULT 4
US-09-490-070A-19
; Sequence 19, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
; White & McAuliffe
; STREET: 1666 K Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:

```

; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; MOLECULE TYPE: protein
; TOPOLOGY: linear
; US-09-490-070A-19
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; Query Match 100.0%; Score 35; DB 4; Length 112;
; Best Local Similarity 100.0%; Pred. No. 1.9;
; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 DVSKRPS 7
; Db 52 DVSKRPS 58
;
; RESULT 5
; US-09-490-153-19
; Sequence 19, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
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; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; MOLECULE TYPE: protein
; TOPOLOGY: linear
; US-09-490-070A-19
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; Query Match 100.0%; Score 35; DB 4; Length 112;
; Best Local Similarity 100.0%; Pred. No. 1.9;
; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Qy 1 DVSKRPS 7
; Db 52 DVSKRPS 58
;
; RESULT 6
; US-09-490-324-19
; Sequence 19, Application US/09490324
; Patent No. 6828422
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; Pack, Peter
; Ilag, Vic
; Ge, Liming
; Moroney, Simon
; Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,324
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769
; FILING DATE: 18-FEB-1998
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; MOLECULE TYPE: protein
; TOPOLOGY: linear
; US-09-490-324-19
;
; Query Match 100.0%; Score 35; DB 4; Length 112;
; Best Local Similarity 100.0%; Pred. No. 1.9;
; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 DVSKRPS 7
; Db 52 DVSKRPS 58
;
; RESULT 7
; US-09-383-667-25
; Sequence 25, Application US/09383667
;
; Query Match 100.0%; Score 35; DB 4; Length 112;
; Best Local Similarity 100.0%; Pred. No. 1.9;
; Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; Qy 1 DVSKRPS 7
; Db 52 DVSKRPS 58
;
; RESULT 7
; US-09-383-667-25
; Sequence 25, Application US/09383667
;
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; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hass, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchhofer, Daniel
; APPLICANT: Suggest, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383,667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 25
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-25

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Query Match      88.6%; Score 31; DB 4; Length 7;
Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 DVS KRPS 7
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DB      1 EVS KRPS 7

```

RESULT 8

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US-09-424-840B-125
; Sequence 125, Application US/09424840B
; Patent No. 6790938
; GENERAL INFORMATION:
; APPLICANT: Escher, Robert F. A.
; TITLE OF INVENTION: ANTI-GPIIb/IIIa RECOMBINANT ANTIBODIES
; FILE REFERENCE: 100564-09049
; CURRENT APPLICATION NUMBER: US/09/424,840B
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: DE 19820663.1
; PRIOR FILING DATE: 1998-05-08
; PRIOR APPLICATION NUMBER: DE 19755227.7
; PRIOR FILING DATE: 1997-12-12
; PRIOR APPLICATION NUMBER: DE 19723904.8
; PRIOR FILING DATE: 1997-06-06
; NUMBER OF SEQ ID NOS: 128
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 125
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-424-840B-125

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Query Match      88.6%; Score 31; DB 4; Length 7;
Best Local Similarity 85.7%; Pred. No. 4.1e+05;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 DVS KRPS 7
        :|||||
DB      1 EVS KRPS 7

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RESULT 9

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US-08-378-939-12
; Sequence 12, Application US/08378939
; Patent No. 5876961
; GENERAL INFORMATION:
; APPLICANT: CROWE, JAMES SCOTT

```

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; APPLICANT: LEWIS, ALAN PETER
; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES
; NUMBER OF SEQUENCES: 46
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ROTHWELL, FIGG, ERNST & KURZ
; STREET: 555 THIRTEENTH ST. N.W.
; CITY: WASHINGTON
; STATE: D. C.
; COUNTRY: U.S.
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/378,939
; APPLICATION NUMBER: US/08/378,939
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/952640
; FILING DATE: 01-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: ERNST, BARBARA G
; REGISTRATION NUMBER: 30,377
; REFERENCE/DOCKET NUMBER: 1808-118
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 783-6040
; TELEFAX: (202) 783-6031
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-378-939-12

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Query Match      88.6%; Score 31; DB 2; Length 235;
Best Local Similarity 85.7%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      1 DVS KRPS 7
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DB      71 EVS KRPS 77

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RESULT 10

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US-08-487-550-10
; Sequence 10, Application US/08487550
; Patent No. 6113898
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,550
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435

```

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ATTORNEY/AGENT INFORMATION:
NAME: Teskin, Robin L.
REGISTRATION NUMBER: 35,030
REFERENCE/DOCKET NUMBER: 012712-131
TELEPHONE: 703-836-6620
TELEFAX: 703-836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-487-550-10

Query Match      88.6%; Score 31; DB 3; Length 236;
Best Local Similarity 71.4%; Pred. No. 33;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
   |:|:|
Db 71 DINKRPS 77

RESULT 11
US-09-526-098-10
; Sequence 10, Application US/09526098
; Patent No. 6492134
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; AND USE THEREOF AS PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/526,098
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/383,916
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-526-098-10

Query Match      88.6%; Score 31; DB 4; Length 236;
Best Local Similarity 71.4%; Pred. No. 33;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
   |:|:|
Db 71 DINKRPS 77

RESULT 12
US-09-383-916-10
; Sequence 10, Application US/09383916
; Patent No. 6709654
; GENERAL INFORMATION:
; APPLICANT: Anderson, Darrell R.
; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC
; TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,
; AND USE THEREOF AS PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS
; IMMUNOSUPPRESSANTS"
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/383,916
; FILING DATE: 26-AUG-1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,550
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Teskin, Robin L.
; REGISTRATION NUMBER: 35,030
; REFERENCE/DOCKET NUMBER: 012712-131
; TELEPHONE: 703-836-6620
; TELEFAX: 703-836-2021
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-383-916-10

Query Match      88.6%; Score 31; DB 4; Length 236;
Best Local Similarity 71.4%; Pred. No. 33;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
   |:|:|
Db 71 DINKRPS 77

RESULT 13
US-09-949-016-7859
; Sequence 7859, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
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;
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7859
; LENGTH: 1039
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7859

Query Match 88.6%; Score 31; DB 4; Length 1039;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRP 6
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Db 915 DVSKRP 920

RESULT 14
US-09-369-364A-13
; Sequence 13, Application US/09369364A
; Patent No. 6391610
; GENERAL INFORMATION:
; APPLICANT: Apte, Suneel
; APPLICANT: Hurekainen, Tiina L.
; APPLICANT: Hirohata, Satoshi
; TITLE OF INVENTION: Nucleic Acids Encoding Zinc Metalloproteases
; FILE REFERENCE: 26473/4007/10-30-00
; CURRENT APPLICATION NUMBER: US/09/369,364A
; CURRENT FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1882
; TYPE: PRT
; ORGANISM: Homo sapiens ADAMTS-9
; FEATURE:
; NAME/KEY: MOD RES
; LOCATION: (468)
; OTHER INFORMATION: Xaa = C
; NAME/KEY: MOD RES
; LOCATION: (521)
; OTHER INFORMATION: Xaa = Y
US-09-369-364A-13

Query Match 88.6%; Score 31; DB 3; Length 1882;
Best Local Similarity 100.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRP 6
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Db 1543 DVSKRP 1548

RESULT 15
US-09-025-769B-33
; Sequence 33, Application US/09025769B
; Patent No. 6300064
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckthun, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

;
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: James F. Haley, Jr., Esq.
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: MORPHO/5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)596-9000
; TELEFAX: (212)596-9090
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 110 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-025-769B-33

Query Match 85.7%; Score 30; DB 3; Length 110;
Best Local Similarity 85.7%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
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Db 52 DVSNRPS 58

Search completed: October 14, 2005, 16:22:03
Job time : 14.7812 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 14, 2005, 16:20:10 ; Search time 49.7656 Seconds
(without alignments)
58.615 Million cell updates/sec

Title: US-10-614-959-14

Perfect score: 35

Sequence: 1 DVSKRPS 7

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Searched: 1859788 seqs, 416717961 residues

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pdb.p*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	35	100.0	99	15	US-10-308-817-98
2	35	100.0	99	15	US-10-453-698-98
3	35	100.0	110	15	US-10-447-331-1
4	35	100.0	111	15	US-10-360-828-61
5	35	100.0	118	18	US-10-916-758-42
6	35	100.0	240	10	US-09-880-748-1898
7	35	100.0	240	15	US-10-293-418-1898
8	35	100.0	241	10	US-09-880-748-2055
9	35	100.0	241	15	US-10-293-418-2055
10	35	100.0	242	18	US-10-981-692-24
11	35	100.0	242	18	US-10-981-692-40
					Sequence 98, Appl
					Sequence 98, Appl
					Sequence 1, Appl
					Sequence 61, Appl
					Sequence 42, Appl
					Sequence 1898, Ap
					Sequence 1898, Ap
					Sequence 2055, Ap
					Sequence 2055, Ap
					Sequence 24, Appl
					Sequence 40, Appl

12	35	100.0	243	10	US-09-880-748-1927	Sequence 1927, Ap
13	35	100.0	243	15	US-10-293-418-1927	Sequence 1927, Ap
14	35	100.0	243	18	US-10-981-692-29	Sequence 29, Appl
15	35	100.0	243	18	US-10-981-692-33	Sequence 33, Appl
16	35	100.0	244	18	US-10-981-692-26	Sequence 26, Appl
17	35	100.0	245	10	US-09-880-748-1926	Sequence 1926, Ap
18	35	100.0	245	15	US-10-293-418-1926	Sequence 1926, Ap
19	35	100.0	245	15	US-10-293-418-3241	Sequence 3241, Ap
20	35	100.0	245	18	US-10-981-692-31	Sequence 31, Appl
21	35	100.0	245	18	US-10-981-692-36	Sequence 36, Appl
22	35	100.0	246	10	US-09-880-748-1913	Sequence 1913, Ap
23	35	100.0	246	10	US-09-880-748-1917	Sequence 1917, Ap
24	35	100.0	246	15	US-10-293-418-1913	Sequence 1913, Ap
25	35	100.0	246	15	US-10-293-418-1917	Sequence 1917, Ap
26	35	100.0	247	10	US-09-880-748-1443	Sequence 1443, Ap
27	35	100.0	247	10	US-09-880-748-1682	Sequence 1682, Ap
28	35	100.0	247	10	US-09-880-748-1685	Sequence 1685, Ap
29	35	100.0	247	10	US-09-880-748-1707	Sequence 1707, Ap
30	35	100.0	247	10	US-09-880-748-1899	Sequence 1899, Ap
31	35	100.0	247	10	US-09-880-748-1928	Sequence 1928, Ap
32	35	100.0	247	10	US-09-880-748-1934	Sequence 1934, Ap
33	35	100.0	247	15	US-10-293-418-1443	Sequence 1443, Ap
34	35	100.0	247	15	US-10-293-418-1682	Sequence 1682, Ap
35	35	100.0	247	15	US-10-293-418-1685	Sequence 1685, Ap
36	35	100.0	247	15	US-10-293-418-1707	Sequence 1707, Ap
37	35	100.0	247	15	US-10-293-418-1899	Sequence 1899, Ap
38	35	100.0	247	15	US-10-293-418-1928	Sequence 1928, Ap
39	35	100.0	247	15	US-10-293-418-1934	Sequence 1934, Ap
40	35	100.0	247	17	US-10-935-290-46	Sequence 46, Appl
41	35	100.0	247	17	US-10-935-290-77	Sequence 77, Appl
42	35	100.0	247	17	US-10-935-290-88	Sequence 88, Appl
43	35	100.0	247	17	US-10-935-290-91	Sequence 91, Appl
44	35	100.0	247	17	US-10-935-290-96	Sequence 96, Appl
45	35	100.0	247	17	US-10-935-290-105	Sequence 105, App

ALIGNMENTS

RESULT 1

US-10-308-817-98

; Sequence 98, Application US/10308817

; Publication No. US20030219861A1

; GENERAL INFORMATION:

; APPLICANT: Rother, Russell

; APPLICANT: Wu, Dayang

; TITLE OF INVENTION: HYBRID ANTIBODIES

; FILE REFERENCE: 1087-37

; CURRENT APPLICATION NUMBER: US/10/308,817

; CURRENT FILING DATE: 2002-12-03

; NUMBER OF SEQ ID NOS: 195

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 98

; LENGTH: 99

; TYPE: PRT

; ORGANISM: human

US-10-308-817-98

Query Match 100.0%; Score 35; DB 15; Length 99;

Best Local Similarity 100.0%; Pred. No. 15;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7

Db 52 DVSKRPS 58

|||||

RESULT 2

US-10-453-698-98

; Sequence 98, Application US/10453698

; Publication No. US20040038308A1

; GENERAL INFORMATION:

; APPLICANT: Rother, Russell

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; TITLE OF INVENTION: HYBRID ANTIBODIES
; FILE REFERENCE: 82 CIP (1087-37 CIP)
; CURRENT APPLICATION NUMBER: US/10/453,698
; CURRENT FILING DATE: 2003-06-03
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 98
; LENGTH: 99
; TYPE: PRT
; ORGANISM: human
US-10-453-698-98

Query Match          100.0%; Score 35; DB 15; Length 99;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 52 DVSKRPS 58

RESULT 3
US-10-447-331-1
; Sequence 1, Application US/10447331
; Publication No. US2003021943A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Ridgway, John B.
; TITLE OF INVENTION: ANTIBODIES FOR CANCER THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS
; FILE REFERENCE: GENENT.122A
; CURRENT APPLICATION NUMBER: US/10/447,331
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: US/09/515,825
; PRIOR FILING DATE: 2000-02-29
; PRIOR APPLICATION NUMBER: 60/122262
; PRIOR FILING DATE: 1999-03-01
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 110
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-447-331-1

Query Match          100.0%; Score 35; DB 15; Length 110;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 52 DVSKRPS 58

RESULT 4
US-10-360-828-61
; Sequence 61, Application US/10360828
; Publication No. US20030206909A1
; GENERAL INFORMATION:
; APPLICANT: Hua, Shaobing
; APPLICANT: Pauling, Michelle H.
; APPLICANT: Zhu, Li
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST MEMBRANE PROTEINS
; FILE REFERENCE: 25636-727
; CURRENT APPLICATION NUMBER: US/10/360,828
; CURRENT FILING DATE: 2003-02-07
; PRIOR APPLICATION NUMBER: US 10/071,866
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/072,301
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 10/133,978
; PRIOR FILING DATE: 2002-04-25
; NUMBER OF SEQ ID NOS: 64

; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 111
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: VL of scFv Ab124
US-10-360-828-61

Query Match          100.0%; Score 35; DB 15; Length 111;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 52 DVSKRPS 58

RESULT 5
US-10-916-758-42
; Sequence 42, Application US/10916758
; Publication No. US20050180977A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Madison, Edwin L.
; TITLE OF INVENTION: ENDOTHELINASE-2 LIGANDS
; FILE REFERENCE: 10280-065001
; CURRENT APPLICATION NUMBER: US/10/916,758
; CURRENT FILING DATE: 2004-08-12
; PRIOR APPLICATION NUMBER: US 60/520,164
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US 60/495,005
; PRIOR FILING DATE: 2003-08-14
; NUMBER OF SEQ ID NOS: 113
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 42
; LENGTH: 118
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated peptide
US-10-916-758-42

Query Match          100.0%; Score 35; DB 18; Length 118;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 52 DVSKRPS 58

RESULT 6
US-09-880-748-1898
; Sequence 1898, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-03-25
; NUMBER OF SEQ ID NOS: 3239
```


; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1898
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1898

Query Match 100.0%; Score 35; DB 10; Length 240;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 181 DVSKRPS 187

RESULT 7

US-10-293-418-1898
; Sequence 1898, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1898
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-293-418-1898

Query Match 100.0%; Score 35; DB 15; Length 240;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 181 DVSKRPS 187

RESULT 8

US-09-880-748-2055
; Sequence 2055, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2055
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-2055

Query Match 100.0%; Score 35; DB 10; Length 241;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 182 DVSKRPS 188

RESULT 9

US-10-293-418-2055
; Sequence 2055, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2055
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-293-418-2055

Query Match 100.0%; Score 35; DB 15; Length 241;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 182 DVSKRPS 188

RESULT 10

US-10-981-692-24
; Sequence 24, Application US/10981692
; Publication No. US2005016377A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.

; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PF590P1
; CURRENT APPLICATION NUMBER: US/10/981,692

; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N015E08 scFv
US-10-981-692-24

Query Match 100.0%; Score 35; DB 18; Length 242;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 182 DVSKRPS 188

RESULT 11
US-10-981-692-40
; Sequence 40, Application US/10981692
; Publication No. US20050163777A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PF590P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N015D10 scFv
US-10-981-692-40

Query Match 100.0%; Score 35; DB 18; Length 242;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 182 DVSKRPS 188

RESULT 12
US-09-880-748-1927
; Sequence 1927, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1927
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1927

Query Match 100.0%; Score 35; DB 10; Length 243;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 183 DVSKRPS 189

RESULT 13
US-10-293-418-1927
; Sequence 1927, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1927
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1927

Query Match 100.0%; Score 35; DB 15; Length 243;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVSKRPS 7
Db 183 DVSKRPS 189

RESULT 14
US-10-981-692-29
; Sequence 29, Application US/10981692
; Publication No. US20050163777A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PF590P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; CURRENT FILING DATE: 2004-11-05

; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N024E07 scFv
US-10-981-692-29

Query Match 100.0%; Score 35; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 183 DVSKRPS 189

RESULT 15
US-10-981-692-33
; Sequence 33, Application US/10981692
; Publication No. US20050163777A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PF590P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N023E01 scFv
US-10-981-692-33

Query Match 100.0%; Score 35; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DVSKRPS 7
Db 183 DVSKRPS 189

Search completed: October 14, 2005, 17:00:44
Job time : 50.7656 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 15:51:19 ; Search time 84.5625 Seconds
(without alignments)
50.310 Million cell updates/sec

Title: US-10-614-959-15
Perfect score: 58
Sequence: 1 AAWDDSLSEFL 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	58	100.0	11	3 AAY79073	Aay79073 Anti-fact
2	58	100.0	104	2 AAR80087	Aar80087 Human der
3	58	100.0	104	2 AAW95485	Aaw95485 Human-der
4	58	100.0	109	4 AAU02544	Aau02544 Anti-adip
5	58	100.0	110	4 AAU02558	Aau02558 Anti-adip
6	58	100.0	110	4 AAU02612	Aau02612 Anti-adip
7	58	100.0	110	4 AAU02627	Aau02627 Anti-adip
8	58	100.0	110	4 AAU02629	Aau02629 Anti-adip
9	58	100.0	111	2 AAW19883	Aaw19883 CEA-speci
10	58	100.0	111	4 AAU02542	Aau02542 Anti-adip
11	58	100.0	111	4 AAU02551	Aau02551 Anti-adip
12	58	100.0	111	4 AAU02585	Aau02585 Anti-adip
13	58	100.0	111	4 AAU02606	Aau02606 Anti-adip
14	58	100.0	242	8 ADG34301	Adg34301 Neurokini
15	58	100.0	242	8 ADG34317	Adg34317 Neurokini
16	58	100.0	243	5 ABP45916	Abp45916 Human Bly
17	58	100.0	243	7 ADG96743	Adg96743 Single ch
18	58	100.0	243	8 ADG34310	Adg34310 Neurokini
19	58	100.0	243	8 ADG34306	Adg34306 Neurokini
20	58	100.0	244	8 ADG34303	Adg34303 Neurokini
21	58	100.0	245	5 ABP45915	Abp45915 Human Bly
22	58	100.0	245	7 ADG96742	Adg96742 Single ch
23	58	100.0	245	7 ADG98057	Adg98057 TNF proli
24	58	100.0	245	8 ADE83862	Ade83862 Chemokine
25	58	100.0	245	8 ADG34308	Adg34308 Neurokini

ALIGNMENTS

RESULT 1
AAV79073
ID AAV79073 standard; peptide; 11 AA.

AC AAV79073;

DT 12-JUN-2000 (first entry)

DE Anti-factor IX/IXa antibody L chain V domain CDR3 amino acid sequence.

XX Complementarity determining region 3; CDR3; antibody; Gla domain;
factor IX/IXa; blood coagulation; deep venous thrombosis; light chain;
arterial thrombosis; unstable angina; post myocardial infarction;
coronary artery bypass graft; CABG; stroke; tumour growth; metastasis;
percutaneous transluminal coronary angioplasty; PTCA; inflammation;
septic shock; hypotension; adult respiratory distress syndrome; ARDS;
arterial fibrillation; disseminated intravascular coagulopathy; DIC.

OS Homo sapiens.

PN WO200012562-A1.

PD 09-MAR-2000.

PF 26-AUG-1999; 99WO-US019453.

PR 28-AUG-1998; 98US-0098233P.

XX 03-MAR-1999; 99US-0122767P.

(GETH) GENENTECH INC.

PI Adams CW, Devaux B, Eaton DL, Hass PE, Judice JK, Kirchhofer D;
Suggett S;

DR WPI; 2000-256595/22.

XX Novel human anti-Factor IX/IXa antibodies against IX/IXa gamma-
carboxyglutamic acid domains useful as anti-coagulant in thrombosis,
stroke, and post myocardial infarction.

XX Claim 8; Fig 2; 84pp; English.

PS This sequence represents a complementarity determining region 3 (CDR3) of
the light chain variable domain of a human anti-factor IX/IXa domain
antibody. Factor IXa is a vitamin K dependent plasma serine protease that
participates in the blood coagulation pathways. The Gla domain of factor
IXa and its zymogen factor IX contains important structural determinants
for interaction with high affinity binding sites on vascular endothelial

26	58	100.0	246	5	ABP45902	Abp45902 Human Bly
27	58	100.0	246	5	ABP45906	Abp45906 Human Bly
28	58	100.0	246	7	ADG96733	Adg96733 Single ch
29	58	100.0	246	7	ADG96729	Adg96729 Single ch
30	58	100.0	245	8	ADE83872	Ade83872 Chemokine
31	58	100.0	247	5	ABP45671	Abp45671 Human Bly
32	58	100.0	247	5	ABP45432	Abp45432 Human Bly
33	58	100.0	247	5	ABP45923	Abp45923 Human Bly
34	58	100.0	247	5	ABP45917	Abp45917 Human Bly
35	58	100.0	247	5	ABP45696	Abp45696 Human Bly
36	58	100.0	247	5	ABP45888	Abp45888 Human Bly
37	58	100.0	247	7	ADG30413	Adg30413 Human GMB
38	58	100.0	247	7	ADG30455	Adg30455 Human GMB
39	58	100.0	247	7	ADG96715	Adg96715 Single ch
40	58	100.0	247	7	ADG96498	Adg96498 Single ch
41	58	100.0	247	7	ADG96744	Adg96744 Single ch
42	58	100.0	247	7	ADG96259	Adg96259 Single ch
43	58	100.0	247	7	ADG96750	Adg96750 Single ch
44	58	100.0	247	7	ADG96523	Adg96523 Single ch
45	58	100.0	247	8	ADE83874	Ade83874 Chemokine

CC cells and platelets. Compositions comprising the antibodies are used for
 CC the treatment or prophylaxis of thrombotic or coagulopathic diseases or
 CC disorders in a mammal for which inhibiting a FIX/IXa mediated event is
 CC indicated, e.g. deep venous thrombosis, arterial thrombosis, unstable
 CC angina, post myocardial infarction, post surgical thrombosis, coronary
 CC artery bypass graft (CABG), percutaneous transluminal coronary
 CC angioplasty (PTCA), stroke, tumour growth, invasion or metastasis,
 CC inflammation, septic shock, hypotension, adult respiratory distress
 CC syndrome (ARDS), arterial fibrillation and disseminated intravascular
 CC coagulopathy (DIC)
 XX
 SQ Sequence 11 AA;

Query Match 100.0%; Score 58; DB 3; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.0022;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDDSLSEFL 11
 DB 1 AAWDDSLSEFL 11
 |||||

RESULT 2
 AAR80087
 ID AAR80087 standard; protein; 104 AA.

XX AAR80087;
 XX
 DT 23-MAY-1996 (first entry)
 XX
 DE Human derived light chain RT3 phage antibody.
 XX
 KW Light chain; RT3; human; catalytic antibody; bacteriophage.
 XX
 OS Homo sapiens.

XX Key Location/Qualifiers
 FT Region 7..15
 FT /note= "framework region 1"
 FT Region 16..28
 FT /note= "complementarity determining region 1"
 FT Region 29..42
 FT /note= "framework region 2"
 FT Region 43..50
 FT /note= "complementarity determining region 2"
 FT Region 51..82
 FT /note= "framework region 3"
 FT Region 83..93
 FT /note= "complementarity determining region 3"
 FT Region 94..104
 FT /note= "framework region 4"

XX WO9527045-A1.
 XX
 XX 12-OCT-1995.
 XX
 XX 30-MAR-1994; 94WO-US003420.
 XX
 XX 30-MAR-1994; 94WO-US003420.
 XX
 XX (IGEN-) IGEN INC.

XX Smith RG, McCafferty J, Chiswell D, Darsley MJ, Fitzgerald K;
 PI Kenten JH, Martin MT, Titmas RC, Williams RO;
 XX
 XX WPI; 1995-358624/46.
 DR N-PSDB; AAT04634.
 XX
 XX Production of catalytic antibodies displayed on phage - by generating a
 PT gene library of antibody-derived domains and expressing it in phage
 PT vectors.
 XX
 XX Disclosure; Fig 20; 133pp; English.

XX AAT04634 encodes AAR80087 human derived light chain RT3 phage antibody.
 CC The DNA was used in the prepn. of catalytic antibody (CA) producing
 CC bacteriophage. The CAs can be used to activate/deactivate a biological
 CC function in an animal by enhancing the rate of cleavage, or formation of
 CC a specific bond within a mol. in vivo
 XX
 SQ Sequence 104 AA;

Query Match 100.0%; Score 58; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 0.023;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDDSLSEFL 11
 DB 83 AAWDDSLSEFL 93
 |||||

RESULT 3
 AAW95485
 ID AAW95485 standard; protein; 104 AA.

XX AAW95485;
 AC
 XX 29-MAR-1999 (first entry)
 XX
 DT Human-derived RT3 phage antibody light chain genetic sequence.
 XX
 DE Catalytic; antibody; phage display; immunising; phage expression vector;
 KW produg; scfv; RT3.
 XX
 OS Homo sapiens.

XX US5855885-A.
 XX
 XX 05-JAN-1999.
 XX
 XX 14-JUL-1994; 94US-00273146.
 XX
 XX 22-JAN-1993; 93US-00007684.

XX (MCCA/) MCCAFFERTY J.
 PA (CHIS/) CHISWELL D.
 PA (DARS/) DARSLEY M J.
 PA (TITM/) TITMAS R C.
 PA (MART/) MARTIN M T.
 PA (KENT/) KENTEN J H.
 PA (SMIT/) SMITH R.
 PA (FITZ/) FITZGERALD K.
 PA (WILL/) WILLIAMS R O.

XX Fitzgerald K, Darsley MJ, Williams RO, Smith R, Martin MT;
 PI Kenten JH, Chiswell D, McCafferty J, Titmas RC;
 XX
 XX WPI; 1999-105036/09.
 DR N-PSDB; AAX00884.

XX Production of catalytic antibodies displayed on bacteriophages -
 PT comprises generating a gene library of antibody-derived domains inserting
 PT coding into a phage expression vector and isolating the catalytic
 PT antibodies.

XX Example; Fig 20B; 117pp; English.

XX The invention relates to methods for producing catalytic antibodies
 CC displayed on a phage. The method comprises: (a) generating a gene library
 CC of antibody-derived domains; (b) inserting coding for the domains into a
 CC phage expression vector; and (c) isolating the catalytic antibodies. The
 CC phage expression vector incorporates a histidine peptide in tandem with a
 CC myc peptide. The catalytic antibodies can be isolated by preparing an
 CC antigen, optionally immunising an animal with the antigen; generating a
 CC library of VH and VL domains from the immunised animal; cloning the VH
 CC and VL domains into a phage expression vector to generate phage display

CC antibodies; selecting phage display antibodies which bind specifically to
 CC the antigen; screening the selected phage display antibodies for
 CC catalytic activity to substrate; and isolating the catalytic antibodies,
 CC where the phage expression vector incorporates a histidine peptide in
 CC tandem with a myc peptide. The processes are used to produce catalytic
 CC antibodies, which can be used for in vivo activation of a prodrug.
 CC Sequences AA02544-489 represent genetic sequences of heavy and light
 CC chains of RT3 specific phage antibodies selected from a naive human phage
 CC antibody library
 XX
 SQ Sequence 104 AA;

Query Match 100.0%; Score 58; DB 2; Length 104;
 Best Local Similarity 100.0%; Pred. No. 0.023;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AA02544
 |||||
 DB 83 AA02544

RESULT 4
 AA02544
 ID AA02544 standard; protein; 109 AA.

XX AC AA02544;

DT 29-AUG-2001 (first entry)

DE Anti-adipocyte monoclonal antibody light chain, FAT 31.

KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KW heart disease; complementarity determining region; CDR.

XX OS Homo sapiens.

XX PN WO200127279-A1.

XX PD 19-APR-2001.

XX PF 11-OCT-2000; 2000WO-CB003900.

XX PR 12-OCT-1999; 99US-0158812P.

XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Edwards BM, Main SH, Vaughan TJ;

XX WPI; 2001-282031/29.

XX DR N-PSDB; AAS03444.

XX Panel of specific binding members of antibody molecules which bind to
 PT whole adipocytes is used in the treatment of obesity and obesity related
 PT diseases.

XX Claim 1; Page 120; 182pp; English.

XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-

CC abdominal fat associated with heart disease
 XX Sequence 109 AA;

Query Match 100.0%; Score 58; DB 4; Length 109;
 Best Local Similarity 100.0%; Pred. No. 0.024;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AA02558
 |||||
 DB 90 AA02558

RESULT 5
 AAU02558
 ID AAU02558 standard; protein; 110 AA.

XX AC AAU02558;

XX DT 29-AUG-2001 (first entry)

XX DE Anti-adipocyte monoclonal antibody light chain, FAT 44.

KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KW heart disease; complementarity determining region; CDR.

XX OS Homo sapiens.

XX PN WO200127279-A1.

XX PD 19-APR-2001.

XX PF 11-OCT-2000; 2000WO-CB003900.

XX PR 12-OCT-1999; 99US-0158812P.

XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Edwards BM, Main SH, Vaughan TJ;

XX WPI; 2001-282031/29.

XX DR N-PSDB; AAS03458.

XX Panel of specific binding members of antibody molecules which bind to
 PT whole adipocytes is used in the treatment of obesity and obesity related
 PT diseases.

XX Claim 1; Page 128-129; 182pp; English.

XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-

XX abdominal fat associated with heart disease
 XX Sequence 110 AA;

Query Match 100.0%; Score 58; DB 4; Length 110;
 Best Local Similarity 100.0%; Pred. No. 0.024;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY      1 AAWDDSLSEFL 11
Db      |||||
        90 AAWDDSLSEFL 100

RESULT 6
AAU02612
ID AAU02612 standard; protein; 110 AA.
XX
AC AAU02612;
XX
DT 29-AUG-2001 (first entry)
XX
DE Anti-adipocyte monoclonal antibody light chain, FAT 99.
XX
KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.
XX
OS Homo sapiens.
XX
PN WO200127279-A1.
XX
PD 19-APR-2001.
XX
PF 11-OCT-2000; 2000WO-GB003900.
XX
PR 12-OCT-1999; 99US-0158812P.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Edwards BM, Main SH, Vaughan TJ;
XX
DR WPI: 2001-282031/29.
DR N-PSDB; AAS03512.
XX
PT Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.
XX
PS Claim 1; Page 163; 182pp; English.
XX
CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease
XX
SQ Sequence 110 AA;

Query Match 100.0%; Score 58; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAWDDSLSEFL 11
Db      |||||
        90 AAWDDSLSEFL 100

RESULT 7
AAU02627
ID AAU02627 standard; protein; 110 AA.
XX
AC AAU02627;
XX
DT 29-AUG-2001 (first entry)
XX
DE Anti-adipocyte monoclonal antibody light chain, FAT 113.
XX
KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
KW heart disease; complementarity determining region; CDR.
XX
OS Homo sapiens.
XX
PN WO200127279-A1.
XX
PD 19-APR-2001.
XX
PF 11-OCT-2000; 2000WO-GB003900.
XX
PR 12-OCT-1999; 99US-0158812P.
XX
PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI Edwards BM, Main SH, Vaughan TJ;
XX
DR WPI: 2001-282031/29.
DR N-PSDB; AAS03527.
XX
PT Panel of specific binding members of antibody molecules which bind to
PT whole adipocytes is used in the treatment of obesity and obesity related
PT diseases.
XX
PS Claim 1; Page 172; 182pp; English.
XX
CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease
XX
SQ Sequence 110 AA;

Query Match 100.0%; Score 58; DB 4; Length 110;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAWDDSLSEFL 11
Db      |||||
        90 AAWDDSLSEFL 100

RESULT 8
AAU02629
ID AAU02629 standard; protein; 110 AA.
XX
AC AAU02629;
XX
DT 29-AUG-2001 (first entry)
XX
DE Anti-adipocyte monoclonal antibody light chain, FAT 113.
XX
KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;

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KW heart disease; complementarity determining region; CDR.
 XX Homo sapiens.
 OS WO200127279-A1.
 PN 19-APR-2001.
 XX 11-OCT-2000; 2000WO-GB003900.
 XX 12-OCT-1999; 99US-0158812P.
 XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX Edwards BM, Main SH, Vaughan TJ;
 XX WPI; 2001-282031/29.
 DR N-PSDB; AAS03529.
 XX Panel of specific binding members of antibody molecules which bind to
 XX whole adipocytes is used in the treatment of obesity and obesity related
 XX diseases.
 XX Claim 1; Page 173; 182pp; English.
 XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
 CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
 CC and heavy chain complementarity determining regions (CDR) of the
 CC invention. The antibodies can be used in the treatment of obesity and
 CC obesity related diseases. The antibodies can be used to deliver drugs or
 CC pro-drugs directly to the fat mass of an obese patient or the antibody
 CC can be used as a therapeutic itself. Antibodies binding specifically to
 CC adipocytes can be used to activate the immune system to destroy the cells
 CC by complement mediated lysis. The antibodies may be labeled with a
 CC detectable label such as radiolabel, fluorescent or chemical group and
 CC used in methods of diagnosis in human subjects e.g. to determine the
 CC presence of adipocyte antigen on the surface of an adipocyte to detect or
 CC determine the presence or level of adipocytes in a cell or tissue sample.
 CC The antibodies can be used as an alternative means of treatment for obese
 CC patients other than undergoing surgery to remove excess fat. Antibodies
 CC for different types of fat deposits can also be produced e.g. intra-
 CC abdominal fat associated with heart disease
 XX Sequence 110 AA;
 SQ
 Query Match 100.0%; Score 58; DB 4; Length 110;
 Best Local Similarity 100.0%; Pred. No. 0.024;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAWDDSLSEFL 11
 Db 90 AAWDDSLSEFL 100
 RESULT 9
 AAU19883
 ID AAU19883 standard; protein; 111 AA.
 XX AAU19883;
 AC
 XX 07-DEC-1997 (first entry)
 DT
 XX CEA-specific antibody CEA1, CEA2, CEA3 VL sequence.
 DE
 XX Carcinoembryonic antigen; CEA; human; antibody; scFv; tumour marker;
 KW lung cancer; breast cancer; colon cancer; adenocarcinoma; diagnosis.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH 23..35
 FT Region /label= CDR1
 FT /note= "complementarity determining region 1"
 FT

FT Region 50..56
 FT /label= CDR2
 FT /note= "complementarity determining region 2"
 FT 90..100
 FT /label= CDR3
 FT /note= "complementarity determining region 3"
 XX
 PN WO9720932-A1.
 XX 12-JUN-1997.
 PD
 XX 09-DEC-1996; 96WO-GB003043.
 XX 07-DEC-1995; 95GB-00025004.
 PR 23-MAY-1996; 96GB-00010824.
 PR 11-OCT-1996; 96GB-00021295.
 XX
 XX (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 PA
 XX Osbourn JK, Allen DJ, McCafferty JG;
 PI WPI; 1997-319779/29.
 XX N-PSDB; AAT72133.
 DR
 XX Specific binding members for human carcinoembryonic antigen - bind to the
 PT A3-B3 extracellular domain of hCEA and are substantially non-cross-
 PT reactive with human liver cells; used for diagnosing cancer.
 XX
 XX Claim 14; Fig 1b; 128pp; English.
 XX This polypeptide sequence comprises the light chain variable region (VL)
 CC of human carcinoembryonic antigen (hCEA)-specific antibodies CEA1, CEA2
 CC and CEA3. VH (AAT72126-32) and VL (AAT72133-35) gene sequences were
 CC obtained for anti-hCEA antibodies CEA1-CEA7 (see AAW19876-85). A claimed
 CC specific binding member (A) comprises an hCEA specific antibody antigen
 CC binding domain that has a dissociation constant for hCEA of less than 1 x
 CC 10⁻⁸ M, is non-cross-reactive with human liver cells, and
 CC preferentially binds to the A3-B3 extracellular domain of hCEA and/or to
 CC cell-associated hCEA over hCEA over soluble hCEA. Preferred (A) include
 CC pairings of VH and VL sequences from CEA1-7, or their CDR sequences, as
 CC well as CEA6 VH and VL variants. (A) is used to detect cells expressing
 CC hCEA, in vivo or in vitro, especially tumour cells for diagnosing cancer,
 CC e.g. adenocarcinoma of the colon, lung or breast
 XX
 SQ Sequence 111 AA;
 Query Match 100.0%; Score 58; DB 2; Length 111;
 Best Local Similarity 100.0%; Pred. No. 0.025;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AAWDDSLSEFL 11
 Db 90 AAWDDSLSEFL 100
 RESULT 10
 AAU02542
 ID AAU02542 standard; protein; 111 AA.
 XX AAU02542;
 AC
 XX 29-AUG-2001 (first entry)
 DT
 XX Anti-adipocyte monoclonal antibody light chain, FAT 30.
 DE
 XX Antibody; adipocyte; heavy chain; light chain; obesity; fat;
 KW heart disease; complementarity determining region; CDR.
 XX Homo sapiens.
 OS
 XX WO200127279-A1.
 PN 19-APR-2001.
 XX

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XX 11-OCT-2000; 2000WO-GB003900.
XX PF
XX DR
XX PR 12-OCT-1999; 99US-0158812P.
XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PI Edwards BM, Main SH, Vaughan TJ;
XX PS
XX DR WPI; 2001-282031/29.
XX N-PSDB; AAS03442.
XX PT Panel of specific binding members of antibody molecules which bind to
XX PT whole adipocytes is used in the treatment of obesity and obesity related
XX PT diseases.
XX PS Claim 1; Page 118-119; 182pp; English.
XX CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
XX CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
XX CC and heavy chain complementarity determining regions (CDR) of the
XX CC invention. The antibodies can be used in the treatment of obesity and
XX CC obesity related diseases. The antibodies can be used to deliver drugs or
XX CC pro-drugs directly to the fat mass of an obese patient or the antibody
XX CC can be used as a therapeutic itself. Antibodies binding specifically to
XX CC adipocytes can be used to activate the immune system to destroy the cells
XX CC by complement mediated lysis. The antibodies may be labeled with a
XX CC detectable label such as radiolabel, fluorescent or chemical group and
XX CC used in methods of diagnosis in human subjects e.g. to determine the
XX CC presence of adipocyte antigen on the surface of an adipocyte to detect or
XX CC determine the presence or level of adipocytes in a cell or tissue sample.
XX CC The antibodies can be used as an alternative means of treatment for obese
XX CC patients other than undergoing surgery to remove excess fat. Antibodies
XX CC for different types of fat deposits can also be produced e.g. intra-
XX CC abdominal fat associated with heart disease
XX CC
XX SQ Sequence 111 AA;
XX Query Match 100.0%; Score 58; DB 4; Length 111;
XX Best Local Similarity 100.0%; Pred. No. 0.025;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AAWDDSLSEFL 11
XX |||||||||
XX Db 90 AAWDDSLSEFL 100
XX
XX RESULT 11
XX AAU02551
XX ID AAU02551 standard; protein; 111 AA.
XX AC AAU02551;
XX XX
XX DT 29-AUG-2001 (first entry)
XX DE Anti-adipocyte monoclonal antibody light chain, FAT 37.
XX KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
XX KW heart disease; complementarity determining region; CDR.
XX OS Homo sapiens.
XX PN WO200127279-A1.
XX PD 19-APR-2001.
XX PF 11-OCT-2000; 2000WO-GB003900.
XX PR 12-OCT-1999; 99US-0158812P.
XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PI Edwards BM, Main SH, Vaughan TJ;
XX

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XX WPI; 2001-282031/29.
XX N-PSDB; AAS03451.
XX PT Panel of specific binding members of antibody molecules which bind to
XX PT whole adipocytes is used in the treatment of obesity and obesity related
XX PT diseases.
XX PS Claim 1; Page 124; 182pp; English.
XX XX
XX CC AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
XX CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
XX CC and heavy chain complementarity determining regions (CDR) of the
XX CC invention. The antibodies can be used in the treatment of obesity and
XX CC obesity related diseases. The antibodies can be used to deliver drugs or
XX CC pro-drugs directly to the fat mass of an obese patient or the antibody
XX CC can be used as a therapeutic itself. Antibodies binding specifically to
XX CC adipocytes can be used to activate the immune system to destroy the cells
XX CC by complement mediated lysis. The antibodies may be labeled with a
XX CC detectable label such as radiolabel, fluorescent or chemical group and
XX CC used in methods of diagnosis in human subjects e.g. to determine the
XX CC presence of adipocyte antigen on the surface of an adipocyte to detect or
XX CC determine the presence or level of adipocytes in a cell or tissue sample.
XX CC The antibodies can be used as an alternative means of treatment for obese
XX CC patients other than undergoing surgery to remove excess fat. Antibodies
XX CC for different types of fat deposits can also be produced e.g. intra-
XX CC abdominal fat associated with heart disease
XX CC
XX SQ Sequence 111 AA;
XX Query Match 100.0%; Score 58; DB 4; Length 111;
XX Best Local Similarity 100.0%; Pred. No. 0.025;
XX Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 AAWDDSLSEFL 11
XX |||||||||
XX Db 91 AAWDDSLSEFL 101
XX
XX RESULT 12
XX AAU02585
XX ID AAU02585 standard; protein; 111 AA.
XX AC AAU02585;
XX XX
XX DT 29-AUG-2001 (first entry)
XX DE Anti-adipocyte monoclonal antibody light chain, FAT 72.
XX KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
XX KW heart disease; complementarity determining region; CDR.
XX OS Homo sapiens.
XX PN WO200127279-A1.
XX PD 19-APR-2001.
XX PF 11-OCT-2000; 2000WO-GB003900.
XX PR 12-OCT-1999; 99US-0158812P.
XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX PI Edwards BM, Main SH, Vaughan TJ;
XX
XX WPI; 2001-282031/29.
XX N-PSDB; AAS03485.
XX PT Panel of specific binding members of antibody molecules which bind to
XX PT whole adipocytes is used in the treatment of obesity and obesity related
XX PT diseases.
XX

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PS Claim 1; Page 146; 182pp; English.

XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody
CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease

XX SQ Sequence 111 AA;

Query Match 100.0%; Score 58; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.025; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0;

QY 1 AAU02606 standard; protein; 111 AA.
DB 90 AAU02606;
|||||

RESULT 13

AAU02606
ID AAU02606 standard; protein; 111 AA.

XX AC AAU02606;

XX DT 29-AUG-2001 (first entry)

XX DE Anti-adipocyte monoclonal antibody light chain, FAT 95.

XX KW Antibody; adipocyte; heavy chain; light chain; obesity; fat;
XX heart disease; complementarity determining region; CDR.

XX OS Homo sapiens.

XX PN WO200127279-A1.

XX PD 19-APR-2001.

XX PF 11-OCT-2000; 2000WO-GB003900.

XX PR 12-OCT-1999; 99US-0158812P.

XX PA (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Edwards BM, Main SH, Vaughan TJ;

XX DR WPI; 2001-282031/29.

XX DR N-PSDB; AAS03506.

XX PT Panel of specific binding members of antibody molecules which bind to
XX whole adipocytes is used in the treatment of obesity and obesity related
XX diseases.

XX PS Claim 1; Page 159; 182pp; English.

XX AAU02501-AAU02635, and AAU02641-AAU02748 represent the amino acid
CC sequences of anti-adipocyte monoclonal antibody heavy chain, light chain,
CC and heavy chain complementarity determining regions (CDR) of the
CC invention. The antibodies can be used in the treatment of obesity and
CC obesity related diseases. The antibodies can be used to deliver drugs or
CC pro-drugs directly to the fat mass of an obese patient or the antibody

CC can be used as a therapeutic itself. Antibodies binding specifically to
CC adipocytes can be used to activate the immune system to destroy the cells
CC by complement mediated lysis. The antibodies may be labeled with a
CC detectable label such as radiolabel, fluorescent or chemical group and
CC used in methods of diagnosis in human subjects e.g. to determine the
CC presence of adipocyte antigen on the surface of an adipocyte to detect or
CC determine the presence or level of adipocytes in a cell or tissue sample.
CC The antibodies can be used as an alternative means of treatment for obese
CC patients other than undergoing surgery to remove excess fat. Antibodies
CC for different types of fat deposits can also be produced e.g. intra-
CC abdominal fat associated with heart disease

XX SQ Sequence 111 AA;

Query Match 100.0%; Score 58; DB 4; Length 111;
Best Local Similarity 100.0%; Pred. No. 0.025; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0;

QY 1 AAU02606 standard; protein; 242 AA.
DB 91 AAU02606;
|||||

RESULT 14

ADG34301
ID ADG34301 standard; protein; 242 AA.

XX AC ADG34301;

XX DT 26-FEB-2004 (first entry)

XX DE Neurokinin B antibody SEQ ID NO:24.

XX KW Antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
XX hypertension; pre-eclampsia; NKB.

XX OS Synthetic.

XX PN WO2003102136-A2.

XX PD 11-DEC-2003.

XX PF 29-MAY-2003; 2003WO-US016802.

XX PR 30-MAY-2002; 2002US-0383802P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Rosen CA, Ruben SM;

XX DR WPI; 2004-053456/05.

XX DR N-PSDB; ADG34282.

XX PT New antibody that specifically binds neurokinin B, useful for preparing a
XX composition for treating or preventing hypertension or pre-eclampsia.

XX PS Claim 2; SEQ ID NO 24; 127pp; English.

XX The invention relates to a novel antibody specifically binding neurokinin
CC B. An antibody of the invention has hypotensive, and gynaecological
CC activity, and may have a use in gene therapy. The antibody is useful for
CC preparing a composition for treating or preventing hypertension or pre-
CC eclampsia. The present sequence is used in the exemplification of the
CC invention.

XX SQ Sequence 242 AA;

Query Match 100.0%; Score 58; DB 8; Length 242;
Best Local Similarity 100.0%; Pred. No. 0.056; Mismatches 0; Indels 0; Gaps 0;
Matches 11; Conservative 0;

QY 1 AAU02606 standard; protein; 242 AA.
DB 91 AAU02606;
|||||

Db 221 AAWDDSLSEFL 231

RESULT 15
ADG34317
ID ADG34317 standard; protein; 242 AA.
XX
AC ADG34317;
XX
DT 26-FEB-2004 (first entry)
XX
DE Neurokinin B antibody SEQ ID NO:40.
XX
KW antibody; neurokinin B; hypotensive; gynaecological; gene therapy;
XX
KW hypertension; pre-eclampsia; NKB.
XX
OS Synthetic.
XX
PN WO2003102136-A2.
XX
PD 11-DEC-2003.
XX
PF 29-MAY-2003; 2003WO-US016802.
XX
PR 30-MAY-2002; 2002US-0383802P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2004-053456/05.
DR N-PSDB; ADG34298.
XX
PT New antibody that specifically binds neurokinin B, useful for preparing a
composition for treating or preventing hypertension or preeclampsia.
XX
PS Claim 2; SEQ ID NO 40; 127pp; English.
XX
CC The invention relates to a novel antibody specifically binding neurokinin
B. An antibody of the invention has hypotensive, and gynaecological
activity, and may have a use in gene therapy. The antibody is useful for
preparing a composition for treating or preventing hypertension or pre-
eclampsia. The present sequence is used in the exemplification of the
invention.
XX
SQ Sequence 242 AA;
Query Match 100.0%; Score 58; DB 8; Length 242;
Best Local Similarity 100.0%; Pred. No. 0.056;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAWDDSLSEFL 11
|||||||
Db 221 AAWDDSLSEFL 231

Search completed: October 14, 2005, 16:12:42
Job time : 84.5625 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:02:59 ; Search time 15.2969 Seconds
(without alignments)
69.190 Million cell updates/sec

Title: US-10-614-959-15
Perfect score: 58
Sequence: 1 AAWDDSLSEFL 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	74.1	98	2 S36048	Ig lambda chain -
2	43	74.1	129	2 S78058	Ig lambda chain pr
3	43	74.1	235	2 S25750	Ig lambda chain -
4	41	70.7	112	1 L1HUMM	Ig lambda chain V-
5	40	69.0	95	2 S49571	Ig lambda chain pr
6	40	69.0	98	2 S36047	Ig lambda chain -
7	40	69.0	98	2 S36046	Ig lambda chain -
8	40	69.0	109	1 L1HUWA	Ig lambda chain V-
9	40	69.0	117	2 S23627	Ig lambda chain pr
10	40	69.0	149	2 S23626	Ig lambda chain V
11	40	69.0	233	2 S25752	Ig lambda chain -
12	40	69.0	234	2 S25757	Ig lambda chain -
13	40	69.0	235	2 S25754	Ig lambda chain -
14	40	69.0	355	2 E87394	conserved hypotet
15	40	69.0	497	2 G95983	probable glycerol
16	40	69.0	502	2 S49113	hypothetical prote
17	40	69.0	4367	1 B54802	dynein heavy chain
18	39	67.2	110	2 S74428	Ig light chain V-J
19	39	67.2	112	2 D44151	Ig lambda chain V
20	39	67.2	130	2 S78057	Ig lambda chain pr
21	39	67.2	397	1 OKB082	protein kinase (EC
22	39	67.2	1995	2 T08166	probable membrane
23	39	67.2	4344	1 A53489	dynein heavy chain
24	38	65.5	210	2 G84751	hypothetical prote
25	38	65.5	329	2 T18622	hypothetical prote
26	38	65.5	423	2 S41289	hypothetical prote
27	38	65.5	443	2 T30619	probable serine/th
28	38	65.5	842	2 B55853	outer membrane ush
29	38	65.5	885	1 WMBY3L	ribonucleoside-dip

ALIGNMENTS

RESULT 1

S36048
Ig lambda chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C:Accession: S36048; S36049
R:Williams, S.C.
submitted to the EMBL Data Library, April 1993
A:Reference number: S36046
A:Accession: S36048
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <WIL>
A:Cross-references: EMBL:Z22189; NID:g312294; PIDN:CAA80199.1; PID:g312295; EMBL:Z22190
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-91/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 43; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 AAWDDSLS 8
Db 90 AAWDDSLS 97
|||||||

RESULT 2

S78058
Ig lambda chain precursor V-J region (clone mAB 67VL) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 19-Nov-1997 #sequence_revision 05-Dec-1997 #text_change 23-Jul-1999
C:Accession: S78058; S23723
R:Harindranath, N.
submitted to the EMBL Data Library, August 1990
A:Reference number: S78051
A:Accession: S78058
A:Molecule type: mRNA
A:Residues: 1-129 <HAR>
A:Cross-references: EMBL:X54446; NID:g37923; PIDN:CAA38313.1; PID:g930121
R:Harindranath, N.; Goldfarb, I.S.; Ikematsu, H.; Buraaturo, S.E.; Wilder, R.L.; Notkins
Int. Immunol. 3, 865-875, 1991
A:Title: Complete sequence of the genes encoding the V(H) and V(L) regions of low- and h
patient.
A:Reference number: S23716; MUID:92031262; PMID:1718404
A:Accession: S23723
A:Molecule type: mRNA
A:Residues: 19-129 <HAW>
A:Cross-references: EMBL:X54446
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-18/Domain: signal sequence (fragment) #status predicted <SIG>

F:19-129/Product: Ig lambda chain (fragment) #status predicted <MAT>
F:33-109/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 43; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDDSL 8
DB 108 AAWDDSL 115

RESULT 3
S25750
Ig lambda chain - human
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C:Accession: S25750
R:Combiato, G.; Klobeck, H.G.
Eur. J. Immunol. 21, 1513-1522, 1991
A:Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lambda
A:Reference number: S16439; MUID:91257162; PMID:1904362
A:Accession: S25750
A>Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-235 <COM>
A:Cross-references: EMBL:X57815; NID:g33729; PIDN:CAA40952.1; PID:g33730
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:150-218/Domain: immunoglobulin homology <IMM>

Query Match 74.1%; Score 43; DB 2; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDDSL 8
DB 109 AAWDDSL 116

RESULT 4
LIHUMM
Ig lambda chain V-I region (Mem) - human
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: A25479
R:Mihaesco, E.; Roy, J.P.; Congy, N.; Peran-Rivat, L.; Mihaesco, C.
Eur. J. Biochem. 150, 349-357, 1985
A:Title: The amino acid sequence of a lambda light chain presenting abnormal physicochem
A:Reference number: A25479; MUID:85257662; PMID:2410269
A:Accession: A25479
A:Molecule type: protein
A:Residues: 1-112 <MIH>
A:Cross-references: UNIPROT:P06887
A>Note: Residues 33-36 and some of the sequenced peptides were positioned by homology
C:Comment: The C region of this chain has the Mcg+ and Kern+ markers.
C:Genetics:
A:Gene: GDB:IGLV@
A:Cross-references: GDB:119342; OMIM:147240
A:Map position: 22q11.2-22q11.2
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IGM, the subunits associate into la
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin; pyroglytamic acid
F:15-92/Domain: immunoglobulin homology <IMM>
F:15/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:22-90/Disulfide bonds: #status predicted

Query Match 70.7%; Score 41; DB 1; Length 112;
Best Local Similarity 63.6%; Pred. No. 3.4;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAWDDSLSEFL 11

DB 91 AAWDDSLDGYV 101

RESULT 5
S49571
Ig lambda chain precursor V region - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 05-Mar-1995 #sequence_revision 12-May-1995 #text_change 23-Jul-1999
C:Accession: S49571
R:Giachino, C.; Padovan, E.; Lanzavecchia, A.
submitted to the EMBL Data Library, November 1994
A:Description: k+l+ dual receptor B cells are present in the human peripheral repertoire
A:Reference number: S49571
A:Accession: S49571
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-95 <GIA>
A:Cross-references: EMBL:246625; NID:g575259; PIDN:CAA86595.1; PID:g575260
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 69.0%; Score 40; DB 2; Length 95;
Best Local Similarity 87.5%; Pred. No. 4.2;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDDSL 8
DB 76 AAWDDSLT 83

RESULT 6
S36047
Ig lambda chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jan-2000
C:Accession: S36047
R:Williams, S.C.
submitted to the EMBL Data Library, April 1993
A:Reference number: S36046
A:Accession: S36047
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <WIL>
A:Cross-references: EMBL:222188; NID:g312291; PIDN:CAA80198.1; PID:g312292
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-91/Domain: immunoglobulin homology <IMM>

Query Match 69.0%; Score 40; DB 2; Length 98;
Best Local Similarity 87.5%; Pred. No. 4.4;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDDSL 8
DB 90 AAWDDSLN 97

RESULT 7
S36046
Ig lambda chain - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C:Accession: S36046
R:Williams, S.C.
submitted to the EMBL Data Library, April 1993
A:Reference number: S36046
A:Accession: S36046
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <WIL>
A:Cross-references: EMBL:222187; NID:g312312; PIDN:CAA80197.1; PID:g312313
C:Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 69.0%; Score 40; DB 2; Length 98;
Best Local Similarity 87.5%; Pred. No. 4.4;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDSLS 8
|||||:
90 AAWDSLS 97

RESULT 8

LIHWA

Ig lambda chain V-I region (Wah) - human

C;Species: Homo sapiens (man)

C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 09-Jul-2004

C;Accession: A01967

R;Takahashi, Y.; Takahashi, N.; Tetaert, D.; Putnam, F.W.

Proc. Natl. Acad. Sci. U.S.A. 80, 3686-3690, 1983

A;Title: Complete covalent structure of a human immunoglobulin D: sequence of the lambda

A;Reference number: A01967; MUID:83221661; PMID:6407018

A;Accession: A01967

A;Molecule type: protein

A;Residues: 1-109 <TAK>

A;Cross-references: UNIPROT:P04208

C;Genetics:

A;Gene: GDB:IGLV@

A;Cross-references: GDB:119342; OMIM:147240

A;Map position: 22q11.2-22q11.2

C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;1-97/Region: V segment

F;15-91/Domain: immunoglobulin homology <IMM>

F;98-109/Region: J segment

F;22-89/Disulfide bonds: #status predicted

Query Match 69.0%; Score 40; DB 1; Length 109;
Best Local Similarity 80.0%; Pred. No. 4.9;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAWDSLSEF 10
|||||:
90 AAWDSLWVF 99

RESULT 9

S23627

Ig lambda chain precursor - human

C;Species: Homo sapiens (man)

C;Date: 19-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

C;Accession: S23627

R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;

J. Exp. Med. 175, 831-842, 1992

A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from b

A;Reference number: S23623; MUID:92156804; PMID:1740665

A;Accession: S23627

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-117 <OLE>

A;Cross-references: EMBL:X59707; NID:g34426; PIDN:CAA42228.1; PID:g34427

C;Genetics:

A;Introns: 16/1

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-110/Domain: immunoglobulin homology <IMM>

Query Match 69.0%; Score 40; DB 2; Length 117;
Best Local Similarity 87.5%; Pred. No. 5.3;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDSLS 8

Db 109 AAWDSLS 116
|||||:

RESULT 10

S23626

Ig lambda chain V region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Jan-2000

C;Accession: S23626

R;Olee, T.; Lu, E.W.; Huang, D.F.; Soto-Gil, R.W.; Deftos, M.; Kozin, F.; Carson, D.A.;

J. Exp. Med. 175, 831-842, 1992

A;Title: Genetic analysis of self-associating immunoglobulin G rheumatoid factors from t

A;Reference number: S23623; MUID:92156804; PMID:1740665

A;Accession: S23626

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-149 <OLE>

A;Cross-references: EMBL:X59706; NID:g34204; PIDN:CAA42227.1; PID:g34205

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;34-110/Domain: immunoglobulin homology <IMM>

Query Match 69.0%; Score 40; DB 2; Length 149;
Best Local Similarity 87.5%; Pred. No. 6.9;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDSLS 8

|||||:

Db 109 AAWDSLS 116

RESULT 11

S25752

Ig lambda chain - human

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C;Accession: S25752

R;Combrato, G.; Klobeck, H.G.

Eur. J. Immunol. 21, 1513-1522, 1991

A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam

A;Reference number: S16439; MUID:91257162; PMID:1904362

A;Accession: S25752

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-233 <COM>

A;Cross-references: EMBL:X57817; NID:g33733; PIDN:CAA40954.1; PID:g33734

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;148-216/Domain: immunoglobulin homology <IMM>

Query Match 69.0%; Score 40; DB 2; Length 233;
Best Local Similarity 87.5%; Pred. No. 11;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDSLS 8

|||||:

Db 107 AAWDSLS 114

RESULT 12

S25757

Ig lambda chain - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C;Accession: S25757

R;Combrato, G.; Klobeck, H.G.

Eur. J. Immunol. 21, 1513-1522, 1991

A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam

A;Reference number: S16439; MUID:91257162; PMID:1904362

A;Accession: S25757

A;Status: preliminary; translation not shown

A;Molecule type: mRNA

A;Residues: 1-234 <COM>
 A;Cross-references: EMBL:X57822; NID:g33743; PIDN:CAA40959.1; PID:g33744
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F:149-217/Domain: immunoglobulin homology <IMM>

Query Match 69.0%; Score 40; DB 2; Length 234;
 Best Local Similarity 87.5%; Pred. No. 11;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSDLS 8
 |||||:
 Db 108 AAWDSDSLN 115

RESULT 13

S25754
 Ig lambda chain - human (fragment)
 C;Species: Homo sapiens (man)
 C;Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
 C;Accession: S25754
 R;Combiato, G.; Klobbeck, H.G.
 Eur. J. Immunol. 21, 1513-1522, 1991
 A;Title: V(lambda) and J(lambda)-C(lambda) gene segments of the human immunoglobulin lam
 A;Reference number: S16439; MUID:91257162; PMID:1904362
 A;Accession: S25754
 A;Status: preliminary; translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-235 <COM>
 A;Cross-references: EMBL:X57819; NID:g33737; PIDN:CAA40956.1; PID:g33738
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F:150-218/Domain: immunoglobulin homology <IMM>

Query Match 69.0%; Score 40; DB 2; Length 235;
 Best Local Similarity 87.5%; Pred. No. 11;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSDLS 8
 |||||:
 Db 108 AAWDSDSLN 115

RESULT 14

E87394
 conserved hypothetical protein CC1169 [imported] - Caulobacter crescentus
 C;Species: Caulobacter crescentus
 C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 C;Accession: E87394
 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
 B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A;Title: Complete Genome Sequence of Caulobacter crescentus.
 A;Reference number: A87249; MUID:21173698; PMID:11259647

A;Accession: E87394
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-355 <STO>
 A;Cross-references: UNIPROT:Q9A925; GB:AE005673; NID:gl3422491; PIDN:AAK23153.1; GSPDB:G
 C;Genetics:
 A;Gene: CC1169

Query Match 69.0%; Score 40; DB 2; Length 355;
 Best Local Similarity 87.5%; Pred. No. 16;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSDLS 8
 :|||||
 Db 138 SAWDSDLS 145

RESULT 15

G95983
 probable glycerol kinase (EC 2.7.1.30) [imported] - Sinorhizobium meliloti (strain 1021)
 C;Species: Sinorhizobium meliloti
 C;Date: 24-Aug-2001 #sequence_revision 24-Aug-2001 #text_change 09-Jul-2004
 C;Accession: G95983
 R;Finan, T.M.; Weidner, S.; Wong, K.; Buhrmester, J.; Chain, P.; Vorholter, F.J.; Hernan
 Proc. Natl. Acad. Sci. U.S.A. 98, 9889-9894, 2001
 A;Title: The complete sequence of the 1,683-kb pSymB megaplasmid from the N2-fixing endo
 A;Reference number: A95842; MUID:21396508; PMID:11481431
 A;Accession: G95983
 A;Status: Preliminary
 A;Molecule type: DNA
 A;Residues: 1-497 <KUR>
 A;Cross-references: UNIPROT:O86033; GB:AL591985; PIDN:CAC49535.1; PID:gl5141022; GSPDB:C
 R;Galibert, F.; Finan, T.M.; Long, S.R.; Puhler, A.; Abola, P.; Ampe, F.; Barloy-Hubler,
 pela, D.; Chain, P.; Cowie, A.; Davis, R.W.; Dreano, S.; Federspiel, N.A.; Fisher, R.F.;
 L.; Hyman, R.W.; Jones, T.
 Science 293, 668-672, 2001
 A;Authors: Kahn, D.; Kahn, M.L.; Kalman, S.; Keating, D.H.; Kiss, E.; Komp, C.; Lelaure,
 hebault, P.; Vandenbol, M.; Vorholter, F.J.; Weidner, S.; Wells, D.H.; Wong, K.; Yeh, K.
 A;Title: The composite genome of the legume symbiont Sinorhizobium meliloti.
 A;Reference number: A96039; MUID:21368234; PMID:11474104
 A;Contents: annotation
 C;Genetics:
 A;Gene: glpK; SMD21009
 A;Genome: plasmid
 C;Superfamily: xylulokinase
 C;Keywords: phosphotransferase

Query Match 69.0%; Score 40; DB 2; Length 497;
 Best Local Similarity 70.0%; Pred. No. 26;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 AAWDSDSEFL 11
 |||||:
 Db 197 AWDDDELTEVL 206

Search completed: October 14, 2005, 16:23:41
 Job time : 16.2969 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 14, 2005, 15:51:44 ; Search time 73.2188 Seconds
(without alignments)
76.932 Million cell updates/sec

Title: US-10-614-959-15
Perfect score: 58
Sequence: 1 AAWDDSLSEFL 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	75.9	108	2 Q96SB0	Q96sb0 homo sapien
2	43	74.1	236	2 Q8NEJ1	Q8nej1 homo sapien
3	43	74.1	628	2 Q6CLT9	Q6clt9 kluyveromyc
4	41	70.7	112	1 LV1H HUMAN	P06887 homo sapien
5	41	70.7	237	2 Q6DHW4	Q6dhw4 homo sapien
6	40	69.0	109	1 LV1F HUMAN	P04208 homo sapien
7	40	69.0	355	2 Q9A925	Q9a925 caulobacter
8	40	69.0	376	1 CBA2 RAT	Q9jkl5 rattus norv
9	40	69.0	381	1 CBA2 HUMAN	Q9npf8 homo sapien
10	40	69.0	381	1 CBA2 MOUSE	O8r2v5 mus musculu
11	40	69.0	497	1 GLPK_RHIME	O86033 rhizobium m
12	40	69.0	502	2 Q48904	Q48904 microcystis
13	40	69.0	1714	1 YP93 CAEEL	Q09475 caenorhabdi
14	40	69.0	4367	1 DYHC NEUCR	P45443 neurospora
15	39	67.2	182	2 Q87GV3	Q87gv3 vibrio para
16	39	67.2	236	2 Q6GMV7	Q6gmv7 homo sapien
17	39	67.2	397	1 KAPI BOVIN	P24256 bos taurus
18	39	67.2	398	2 Q7Z3M1	Q7z3m1 homo sapien
19	39	67.2	578	2 Q8W0B5	Q8w0b5 oryza sativ
20	39	67.2	751	2 Q6C0Z1	Q6c0z1 yarrowia li
21	39	67.2	894	2 Q74B13	Q74b13 geobacter s
22	39	67.2	969	2 Q7RY83	Q7ry83 neurospora
23	39	67.2	1466	2 Q98TR8	Q98tr8 bufo bufo
24	39	67.2	1995	1 YCX7_CHLRE	P36495 chlamydomon
25	39	67.2	4344	1 DYHC EMENI	P45444 emeritella
26	38	65.5	170	2 Q73YE0	Q73ye0 mycobacteri
27	38	65.5	215	2 Q67NP3	Q67np3 symbiobacte
28	38	65.5	244	2 Q31358	Q31358 brachydanio
29	38	65.5	252	2 Q631V6	Q631v6 bacillus ce
30	38	65.5	252	2 Q72Y69	Q72y69 bacillus ce
31	38	65.5	252	2 Q815W5	Q815w5 bacillus ce

32 38 65.5 252 2 Q81X10 Q81x10 bacillus an
33 38 65.5 252 2 Q6HBP1 Q6hbp1 bacillus th
34 38 65.5 299 2 Q74E50 Q74e50 geobacter s
35 38 65.5 302 1 DAPA_XANAC Q8pln5 xanthomonas
36 38 65.5 329 1 SPA3_CAEEL Q03205 caenorhabdi
37 38 65.5 348 2 Q9F6D9 Q9f6d9 streptomyce
38 38 65.5 395 2 Q6R8A6 Q6r8a6 sodalis glo
39 38 65.5 443 2 Q76S23 Q76sz3 molluscum c
40 38 65.5 443 2 Q83155 Q83155 molluscum c
41 38 65.5 496 2 Q9B091 Q9b091 mycobacteri
42 38 65.5 514 2 Q7WZ48 Q7wz48 nonomurae
43 38 65.5 605 1 FLB1_CANAL Q9wuf6 candida alb
44 38 65.5 842 1 AGC1_ECOLI P46005 escherichia
45 38 65.5 869 1 RIR3_YEAST P21672 saccharomyc

ALIGNMENTS

RESULT 1

Q96SB0 ID Q96SB0 PRELIMINARY; PRT; 108 AA.
AC Q96SB0;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Anti-streptococcal/anti-mycosin immunoglobulin lambda light chain
DE variable region (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98375893; PubMed=9712075;
RA Adderson E.E., Shikhan A.R., Ward K.E., Cunningham M.W.;
RT "Molecular analysis of polyclonal antibodies from
RT rheumatic carditis: human anti-N-acetylglucosamine/anti-mycosin
RT antibody V region genes.";
RL J. Immunol. 161:2020-2031(1998).
DR EMBL; U96394; AB68783.1; -.
DR PDB; 1KU4; Model; L-I-108.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON_TER
SQ SEQUENCE 108 AA; 11594 MW; F4B5DC478A043F48 CRC64;

Query Match 75.9%; Score 44; DB 2; Length 108;
Best Local Similarity 72.7%; Pred. No. 3.1;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 AAWDDSLSEFL 11
|||
Db 90 AAWDDRLSGFM 100

RESULT 2

Q8NEJ1 ID Q8NEJ1 PRELIMINARY; PRT; 236 AA.
AC Q8NEJ1;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;

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RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Altshul S.P., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gnanaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettaman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC030984; AAH30984.1; -.
DR HSSP; P01703; 7EAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig.cl.
DR InterPro; IPR003006; Ig.MHC.
DR InterPro; IPR003596; Ig.v.
DR Pfam; PF07654; C1-set; I.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 2.
DR PROSITE; PS00290; IG.MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 25024 MW; 1703B77942630E08 CRC64;

Query Match 74.1%; Score 43; DB 2; Length 236;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAADSDLS 8
DB 109 AAADSDLS 116
|||||

RESULT 3
Q6CLT9 PRELIMINARY; PRT; 628 AA.
AC Q6CLT9;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Similar to sp|Q9HFC6|Yarrowia lipolytica Calnexin.
GN ORFNames=KLA0F00462g;
OS Kluyveromyces lactis NRRL Y-1140.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=284590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-1140;
RG Genolevures;
RA Dujon B., Sherman D., Fischer G., Durrens P., Casaregola S.,
RA Lafontaine I., de Montigny J., Marck C., Neuveglise C., Talla E.,
RA Goffard N., Frangul L., Aigle M., Anthouard V., Babour A., Barbe V.,
RA Barnay S., Blanchin S., Beckerich J.M., Beyne E., Bleykasten C.,
RA Boissrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,

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RA Nicaud J.M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.P., Straub M.L., Suleau A.,
RA Swennene D., Tekia F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic I., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Wincker P., Souciet J.L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44(2004).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL Y-1140;
RA Genoscope;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; CR382126; CAG97807.1; -.
DR GO; GO:0005514; F:calcium ion storage activity; IEA.
DR InterPro; IPR001580; Calret/calnex.
DR InterPro; IPR008985; Cona_like_lec_gl.
DR Pfam; PF00262; Calreticulin; 1.
DR PRINTS; PR00626; CALRETICULIN.
DR PRODOM; PD001866; Calret/calnex; 1.
DR PROSITE; PS00803; CALRETICULIN_1; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 1.
DR PROSITE; PS00805; CALRETICULIN_REPEAT; 1.
SQ SEQUENCE 628 AA; 70981 MW; B0D8A6D1A64644EE CRC64;

Query Match 74.1%; Score 43; DB 2; Length 628;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 WDDSLSEFL 11
DB 309 WDDSLSEFL 317
|||||

RESULT 4
LV1H HUMAN
ID LV1H HUMAN STANDARD; PRT; 112 AA.
AC P06887;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-I region MEM.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=85257662; PubMed=2410269;
RA Mihaesco E., Roy J.P., Congy N., Peran-Rivat L., Mihaesco C.;
RT "The amino acid sequence of a lambda light chain presenting abnormal
RT physicochemical and antigenic features.";
RL Eur. J. Biochem. 150:349-357(1985).
CC -!- MISCELLANEOUS: Residues 33-36 and some of the sequenced peptides
CC were positioned by homology.
CC -!- MISCELLANEOUS: The C region of this chain has the Mcg+ and Kern+
CC markers.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A25479; LIHUM.
DR HSSP; P01703; 7PAB.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region;
KW Monoclonal antibody; Pyridolone carboxylic acid.
FT DOMAIN 1 106 Ig-like.
FT MOD_RES 1 1 Pyridolone carboxylic acid.
FT DISULFID 22 90 By similarity.
FT NON_TER 112 112

```

SQ SEQUENCE 112 AA; 11789 MW; 748124F079CFFB84 CRC64;

Query Match 70.7%; Score 41; DB 1; Length 112;
Best Local Similarity 63.6%; Pred. No. 12;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAWDSLSEFL 11
|||||:
91 AAWDSLQGYV 101

RESULT 5

Q6DHW4 PRELIMINARY; PRT; 237 AA.
AC Q6DHW4
DT 25-OCT-2004 (TRENBLrel. 28, Created)
DT 25-OCT-2004 (TRENBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TRENBLrel. 28, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.

RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Scheen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan K., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Kryzyski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.

RC TISSUE=Primary B-Cells;
RA Strausberg R.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBSJ databases.
DR EMBL; BC075843; AAH5843.1; -;
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG cl.
DR InterPro; IPR003006; IG MHC.
DR InterPro; IPR003596; IG V.
DR Pfam; PF07654; Cl-set; 1.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 2.
DR SMART; SM00407; IGcl; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 2.
DR PROSITE; PS00290; IG MHC; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 237 AA; 25108 MW; 6814170F7E784825 CRC64;

Query Match 70.7%; Score 41; DB 2; Length 237;
Best Local Similarity 87.5%; Pred. No. 26;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDSL 8

Db 109 AAWDSMS 116
|||||:
LVLF HUMAN

RESULT 6
ID LVLF HUMAN STANDARD; PRT; 109 AA.
AC P04208;
DT 20-MAR-1987 (Rel. 04, Created)
DT 20-MAR-1987 (Rel. 04, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Ig lambda chain V-I region WAH.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=83221661; PubMed=6407018;
RA Takahashi Y., Takahashi N., Tetaert D., Putnam F.W.;
RT "Complete covalent structure of a human immunoglobulin D: sequence of
the lambda light chain.";
EL Proc. Natl. Acad. Sci. U.S.A. 80:3686-3690 (1983).
DR PIR; A01967; LIHWA.
DR HSSP; P01703; 7FAB.

DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Direct protein sequencing; Immunoglobulin V region.
FT DOMAIN 1 97 V segment.
FT DOMAIN 98 109 J segment.
FT DISULFID 22 89 By similarity.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11725 MW; B17785F6A8DF9BAC CRC64;

Query Match 69.0%; Score 40; DB 1; Length 109;
Best Local Similarity 80.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AAWDSLSEFL 10
|||||:
90 AAWDSLWVF 99

RESULT 7

Q9A925 PRELIMINARY; PRT; 355 AA.
ID Q9A925
AC Q9A925;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Hypothetical protein CC1169.
GN OrderedLocustNames=CC1169;
OS Caulobacter crescentus.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacterales;
OC Caulobacteraceae; Caulobacter.
OX NCBI_TaxID=155892;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19089 / CB15;
RX MEDLINE=21173698; PubMed=11259647; DOI=10.1073/pnas.061029298;
RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,
RA Eisen J.A., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,
RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,
RA Kolonay J.F., Smit J., Craven M.B., Khouri H.M., Shetty J.,
RA Berry K.J., Utterback T.R., Tran K., Wolf A.M., Vamathevan J.J.,
RA Ermolaeva M.D., White O., Salzberg S.L., Venter J.C., Shapiro L.,

RA Fraser C.M.;
 RT "Complete genome sequence of *Caulobacter crescentus*.";
 RL Proc. Natl Acad. Sci. U.S.A. 98:4136-4141(2001).
 DR EMBL; AB005795; AK23153.1; -;
 DR PIR; E87394; E87394.
 DR TIGR; CC1169; -;
 DR InterPro; IPR011251; Luciferase like.
 DR Pfam; PF00296; Bac_luciferase; 1.
 KW Complete proteome; Hypothetical protein.
 SQ SEQUENCE 355 AA; 38552 MW; 3C4AEF42825E5567 CRC64;

Query Match 69.0%; Score 40; DB 2; Length 355;
 Best Local Similarity 87.5%; Pred. No. 63;
 Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDDSL 8
 :|||||||
 Db 138 SAWDDSL 145

RESULT 8
 CE2A2_RAT STANDARD; PRT; 376 AA.
 ID CE2A2_RAT
 AC Q9JKL5;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Centaurin alpha 2.
 GN Names=Cent2;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A., INTERACTION WITH PTDINS(4,5)P2, PTDINS(3,4,5)P3
 AND INS(1,3,4,5)P4, TISSUE SPECIFICITY, AND MUTAGENESIS OF ARG-151 AND
 ARG-275.
 RC TISSUE=Adipocyte;
 RX MEDLINE=22012451; PubMed=12018390;
 RA Whitley P., Gibbard A.M., Koumanov F., Oldfield S., Kilgour E.E.,
 Prestwich G.D., Holman G.D.;
 RT "Identification of centaurin-alpha2: a phosphatidylinositol-binding
 protein present in fat, heart and skeletal muscle.";
 RL Eur. J. Cell Biol. 81:222-230(2002).
 CC -!- FUNCTION: GTPase-activating protein for the ADP ribosylation
 factor family (Potential).
 CC -!- SUBUNIT: Binds phosphatidylinositol 4,5-bisphosphate,
 phosphatidylinositol 3,4,5-trisphosphate (PtdInsP3) and inositol
 1,3,4,5-tetrakisphosphate (InsP4). Binding of phosphatidylinositol
 3,5-bisphosphate and phosphatidylinositol 3,4-bisphosphate occurs
 at a much lower affinity. Possesses a stoichiometry of two binding
 sites for InsP4 with identical affinity (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Constitutively associated with
 the plasma membrane. Excluded from the nucleus (By similarity).
 CC -!- TISSUE SPECIFICITY: Expressed in many tissues, with highest levels
 in fat, heart and skeletal muscle. Also detected in kidney, liver
 and lung.
 CC -!- SIMILARITY: Contains 1 Arf-GAP domain.
 CC -!- SIMILARITY: Contains 2 PH domains.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
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 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; AJ238993; CAB88403.1; -;
 DR RGD; 708487; LOC56826.
 DR InterPro; IPR001184; hRIP_like.
 DR InterPro; IPR001849; PH.
 DR InterPro; IPR011036; PH_related.

DR Pfam; PF01412; ArfGap; 1.
 DR Pfam; PF00169; PH; 2.
 DR PRINTS; SM00405; REVINTRACTNG.
 DR SMART; SM00105; ArfGap; 1.
 DR SMART; SM00233; PH; 2.
 DR PROSITE; PS01115; ARFGAP; 1.
 DR PROSITE; PS50003; PH_DOMAIN; 2.
 KW GTPase activation; Metal-binding; Repeat; Zinc; Zinc-finger.
 FT DOMAIN 9 130 Arf-GAP.
 FT ZN_FING 25 48 C4-type.
 FT DOMAIN 131 232 PH 1.
 FT DOMAIN 254 360 PH 2.
 FT MUTAGEN 151 151 R->C: Almost complete loss of InsP4
 binding.
 FT MUTAGEN 275 275 R->C: No loss of InsP4 binding. Almost
 complete loss of InsP4 binding; when
 associated with C-151.
 SQ SEQUENCE 376 AA; 43524 MW; E357392F38F07166 CRC64;

Query Match 69.0%; Score 40; DB 1; Length 376;
 Best Local Similarity 66.7%; Pred. No. 67;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 WDDSLSEPL 11
 |||||:
 Db 69 WDDSNVEFM 77

RESULT 9
 CE2A2_HUMAN STANDARD; PRT; 381 AA.
 ID CE2A2_HUMAN
 AC Q9NPF8; O8N4Q6; Q96SD5;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Centaurin alpha 2.
 GN Name=CENTA2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=22012451; PubMed=12018390;
 RA Whitley P., Gibbard A.M., Koumanov F., Oldfield S., Kilgour E.E.,
 Prestwich G.D., Holman G.D.;
 RT "Identification of centaurin-alpha2: a phosphatidylinositol-binding
 protein present in fat, heart and skeletal muscle.";
 RL Eur. J. Cell Biol. 81:222-230(2002).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RX MEDLINE=20304757; PubMed=10843809; DOI=10.1006/geno.2000.6179;
 RA Jenné D.E., Tinschert S., Stegmann E., Reimann H., Nurnberg P.,
 Horn D., Naumann I., Buske A., Thiel G.;
 RT "A common set of at least 11 functional genes is lost in the majority
 of NF1 patients with gross deletions.";
 RL Genomics 66:93-97(2000).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RA Bertsch U., Illies C., Mayr G.W.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A. (ISOFORM 2).
 RC TISSUE=Leukocyte;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haiech F.,
 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
EL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP INTERACTION WITH PTINS(3,4,5)P3 AND INS(1,3,4,5)P4, TISSUE
RP SPECIFICITY, AND SUBCELLULAR LOCATION.
RX PubMed=14690521;
RT "Identification of gene structure and subcellular localization of
RT human centaurin alpha 2, and p421P4, a family of two highly
RT homologous, Ins 1,3,4,5-P4-/Ptdins 3,4,5-P3-binding, adapter
RT proteins.";
RL J. Neurochem. 88:326-336(2004).
CC -!- FUNCTION: GTPase-activating protein for the ADP ribosylation
CC factor family (Potential).
CC -!- SUBUNIT: Binds phosphatidylinositol 3,4,5-trisphosphate (PtdInsP3)
CC and inositol 1,3,4,5-tetrakisphosphate (InsP4). Possesses a
CC stoichiometry of two binding sites for InsP4 with identical
CC affinity.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Constitutively associated with
CC the plasma membrane. Excluded from the nucleus.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=Q9NPF8-1; Sequence=Displayed;
CC Name=2;
CC IsoId=Q9NPF8-2; Sequence=VSP_011180;
CC Note=May be due to a competing acceptor splice site. No
CC experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Highly expressed in placenta, spleen, kidney,
CC skeletal muscle and adrenal gland. Weakly expressed in thyroid,
CC liver, heart, lung, small intestine, peripheral blood leukocytes.
CC Not detected in spinal cord, brain, stomach, trachea, colon, lymph
CC node and bone marrow.
CC -!- SIMILARITY: Contains 1 Arf-GAP domain.
CC -!- SIMILARITY: Contains 2 PH domains.
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CC or send an email to license@isb-sib.ch).
DR EMBL; AJ238994; CAB88383.1; -;
DR EMBL; AJ272195; CAB77265.1; -;
DR EMBL; AJ242782; CAC40651.1; -;
DR EMBL; BC033758; AAH33758.1; -;
DR Genew; HGNC:16487; CENTA2.
DR H-InvDB; HIX0013699; -;
DR MIM; 608635; -;
DR InterPro; IPR001164; hrip_like.
DR InterPro; IPR001849; PH_.
DR InterPro; IPR011036; PH_related.
DR Pfam; PF04112; ArfGAP; 1.
DR Pfam; PF00169; PH; 2.
DR PRINTS; PR00405; REVINTRACNG.
DR SMART; SM00105; ArfGAP; 1.
DR SMART; SM00233; PH; 2.
DR PROSITE; PS01115; ARFGAP; 1.
DR PROSITE; PS00003; PH_DOMAIN; 2.
KW Alternative splicing; GTPase activation; Metal-binding; Repeat; Zinc;
KW Zinc-finger.

FT DOMAIN 9 131 Arf-GAP.
FT ZN_FING 25 48 C4-type.
FT DOMAIN 132 233 PH 1.
FT DOMAIN 255 361 PH 2.
FT VARSPLIC 269 Missing (in isoform 2).
FT CONFLICT 12 12 Missing (in isoform 2).
FT CONFLICT 12 12 Missing (in isoform 2).
SQ SEQUENCE 381 AA; 44348 MW; 4FAE208072A92C01 CRC64;
L -> P (in Ref. 3).
Query Match 69.0%; Score 40; DB 1; Length 381;
Best Local Similarity 66.7%; Pred. No. 68;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 3 WDDSLSEFL 11
Db 69 WDDSIIVEFM 77
RESULT 10
CEA2 MOUSE
ID CEA2 MOUSE STANDARD; PRT; 381 AA.
AC Q8R2V5;
DT 25-OCT-2004 (Rel. 45, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Centaurin alpha 2.
GN Name=Cent2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVB/N; TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: GTPase-activating protein for the ADP ribosylation
CC factor family (Potential).
CC -!- SUBUNIT: Binds phosphatidylinositol 3,4,5-trisphosphate (PtdInsP3)
CC and inositol 1,3,4,5-tetrakisphosphate (InsP4). Possesses a
CC stoichiometry of two binding sites for InsP4 with identical
CC affinity (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic. Constitutively associated with
CC the plasma membrane. Excluded from the nucleus (By similarity).
CC -!- SIMILARITY: Contains 1 Arf-GAP domain.
CC -!- SIMILARITY: Contains 2 PH domains.
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CC -----
DR EMBL; BC027165; AAH27165.1; -.
DR MGI; MGI:2663075; Centa2.
DR InterPro; IPR001164; hRIP_like.
DR InterPro; IPR001849; PH.
DR InterPro; IPR011036; PH_related.
DR Pfam; PF01412; ArfGAP; 1.
DR Pfam; PF00169; PH; 2.
DR PRINTS; PR00405; REVINTRACTING.
DR SMART; SM00105; ArfGAP; 1.
DR SMART; SM00233; PH; 2.
DR PROSITE; PS50115; ARFGAP; 1.
DR PROSITE; PS50003; PH DOMAIN; 2.
KW GTPase activation; Metal-binding; Repeat; Zinc; Zinc-finger.
FT DOMAIN 9 132 Arf-GAP.
FT ZN_FING 25 48 C4-type.
FT DOMAIN 132 233 PH 1.
FT DOMAIN 255 361 PH 2.
SQ SEQUENCE 381 AA; 43989 MW; 2E504CEFOACD84D5 CRC64;

Query Match 69.0%; Score 40; DB 1; Length 381;
Best Local Similarity 66.7%; Pred. No. 68;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 WDDSLSEFL 11
   |||||:|
Db 69 WDDSMVEFM 77

RESULT 11
ID GLPK RHIME STANDARD; PRT; 497 AA.
AC O86033;
DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Glycerol kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase)
DE (Glycerokinase) (GK).
GN Name=glpK; OrderedLocustNames=RB1135; ORFNames=SMb21009;
OS Rhizobium meliloti (Sinorhizobium meliloti).
OG Plasmid pSymb (megaplasmid 2).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
OX NCBI_TaxID=382;
RN [1]_TaxID=382;
RP SEQUENCE FROM N.A.
RC STRAIN=1021;
RX MEDLINE=21396508; PubMed=11481431; DOI=10.1073/pnas.161294698;
RA Finan T.M., Weidner S., Wong K., Buhrmester J., Chain P.,
RA Vorhoelter F.J., Hernandez-Lucas I., Becker A., Cowie A., Gouzy J.,
RA Golding B., Puehler A.;
RT "The complete sequence of the 1,683-kb pSymb megaplasmid from the N2-
RT fixing endosymbiont Sinorhizobium meliloti."
RL Proc. Natl. Acad. Sci. U.S.A. 98:9889-9894(2001).
RN [2]
RP SEQUENCE OF 1-59 FROM N.A.
RC STRAIN=SU47 / 1021;
RX MEDLINE=99121023; PubMed=9922248;
RA Anuja P., Charles T.C.;
RT "Poly-3-hydroxybutyrate degradation in Rhizobium (Sinorhizobium)
RT meliloti: isolation and characterization of a gene encoding 3-
RT hydroxybutyrate dehydrogenase."
RL J. Bacteriol. 181:849-857(1999).
CC -|- FUNCTION: Key enzyme in the regulation of glycerol uptake and
CC metabolism.
CC -|- CATALYTIC ACTIVITY: ATP + glycerol = ADP + sn-glycerol 3-
CC phosphate.
CC -|- PATHWAY: Glycerol utilization; rate-limiting step.
CC -|- SIMILARITY: Belongs to the fucokinase / gluconokinase /
CC glycerokinase / xylulokinase family.
CC -----
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CC -----
DR EMBL; AL591985; CAC49535.1; -.
DR EMBL; AF080548; AAD12735.1; -.
DR PIR; G95983; G95983.
DR HSSP; P08859; 1GLC.
DR HAMAP; MF_00186; -.
DR InterPro; IPR000577; FGGY_kin.
DR InterPro; IPR005999; Glycerol_kin.
DR Pfam; PF02782; FGGY_C; 1.
DR Pfam; PF00370; FGGY_N; 1.
DR TIGRfam; TIGR01311; glycerol_kin; 1.
DR PROSITE; PS00933; FGGY_KINASES_1; FALSE_NEG.
DR PROSITE; PS00445; FGGY_KINASES_2; 1.
KW ATP-binding; Complete proteome; Glycerol metabolism; Kinase; Plasmid;
KW Transferase.
FT NP_BIND 153 165 ATP (Probable).
SQ SEQUENCE 497 AA; 54419 MW; 42D3428335ACC2B7 CRC64;

Query Match 69.0%; Score 40; DB 1; Length 497;
Best Local Similarity 70.0%; Pred. No. 90;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 AWDDSLSEFL 11
   |||||:|
Db 197 AWDDDELTEVL 206

RESULT 12
Q48904 PRELIMINARY; PRT; 502 AA.
ID Q48904;
AC Q48904;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE ORF2.
OS Microcystis aeruginosa.
OC Bacteria; Cyanobacteria; Chroococcales; Microcystis.
OX NCBI_TaxID=1126;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HUB 5-2-4;
RA Juerchott K., Boerner T.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z28337; CAA82191.1; -.
DR PIR; S49113; S49113.
DR InterPro; IPR000345; CytC_heme_BS.
DR InterPro; IPR007936; VirE.
DR Pfam; PF05272; VirE; 1.
DR PROSITE; PS00190; CYTOCHROME_C; UNKNOWN 1.
SQ SEQUENCE 502 AA; 58859 MW; 98B61D5C214520E6 CRC64;

Query Match 69.0%; Score 40; DB 2; Length 502;
Best Local Similarity 60.0%; Pred. No. 91;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 AWDDSLSEFL 11
   :|||:|
Db 434 SWEDSLAEFL 443

RESULT 13
YPS3_CABEL STANDARD; PRT; 1714 AA.
ID YPS3_CABEL
AC Q09475;
DT 01-NOV-1995 (Rel. 32, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Putative helicase C28H8.3 (EC 3.6.1.-).

```

GN ORFNames=C28H8.3;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematozoa; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=99069613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology";
RL Science 282:2012-2018 (1998).
RN [2]
RP REVISIONS.
RA Waterston R.;
RL Submitted (Sep-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- SIMILARITY: Belongs to the helicase family. SKI2 subfamily.
CC -----
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CC -----
CC EMBL; U20861; AAA62291.2; -;
DR WormBase; WBGene00016194; C28H8.3.
DR WormPep; C28H8.3; C829195.
DR InterPro; IPR001410; DEAD.
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; Helicase_C; 1.
DR SMART; SM00487; DEXDC; 1.
DR TIGRfam; TIGR01870; cas TM1810; 2.
KW ATP-binding; Helicase; Hydrolase; Hypothetical protein;
KW Nuclear protein.
FT NP_BIND 607 614 ATP (Potential).
FT NP_BIND 806 813 ATP (Potential).
FT SITE 913 916 DEVH box.
SQ SEQUENCE 1714 AA; 194095 MW; 0936764D27C7EFAD CRC64;
Query Match 69.0%; Score 40; DB 1; Length 1714;
Best Local Similarity 88.9%; Pred. No. 3.4e-02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 AAWDSLSE 9
Db 5 AAWDSDSSE 13
RESULT 14
DYHC NEUCR STANDARD; PRT; 4367 AA.
AC P45443; Q7RVH1;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Dynein heavy chain, cytosolic (DYHC).
GN Name=ro-1; ORFNames=NCU06976.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=74-OR23-1A / FGSC 987;
RX MEDLINE=95014704; PubMed=7929559; DOI=10.1083/jcb.127.1.139;
RA Plamann M., Minke P.F., Tinsley J.H., Bruno K.S.;
RT "Cytoplasmic dynein and actin-related protein Arp1 are required for

normal nuclear distribution in filamentous fungi."; J. Cell Biol. 127:139-149 (1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=74-OR23-1A / FGSC 987;
RX PubMed=12712197; DOI=10.1038/nature01554;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Reiman B.,
RA Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Tanakiev P., Bell-Pedersen D., Nelson M.A.,
RA Werner-Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L.,
RA Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes H.-W., Staben C.,
RA Marcotte E., Greenberg D., Roy A., Foley K., Naylor J.,
RA Stange-Thomann N., Barrett R., Gnerre S., Kamal M., Kamysseles M.,
RA Mauceli E., Bielek C., Rudd S., Frisman D., Krystofova S.,
RA Ramussen C., Metzberg R.L., Perkins D.D., Kroken S., Cogoni C.,
RA Macino G., Catchside D., Li W., Pratt R.J., Osmari S.A.,
RA DeSouza C.P., Glass L., Orbach M.J., Berglund J.A., Voelker R.,
RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Eboile D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
RT "The genome sequence of the filamentous fungus Neurospora crassa";
RL Nature 422:859-868 (2003).
CC -1- FUNCTION: Cytoplasmic dynein acts as a motor for the intracellular
CC retrograde motility of vesicles and organelles along microtubules.
CC Dynein has ATPase activity; the force-producing power stroke is
CC thought to occur on release of ADP. Required to maintain uniform
CC nuclear distribution in hyphae.
CC -1- SUBUNIT: Consists of at least two heavy chains and a number of
CC intermediate and light chains.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- DOMAIN: Dynein heavy chains probably consist of an N-terminal stem
CC (which binds cargo and interacts with other dynein components),
CC and the head or motor domain. The motor contains six tandemly-
CC linked AAA domains in the head, which form a ring. A stalk-like
CC structure (formed by two of the coiled coil domains) protrudes
CC between AAA 4 and AAA 5 and terminates in a microtubule-binding
CC site. A seventh domain may also contribute to this ring; it is not
CC clear whether the N-terminus or the C-terminus forms this extra
CC domain. There are four well-conserved and two non-conserved ATPase
CC sites, one per AAA domain. Probably only one of these (within AAA
CC 1) actually hydrolyzes ATP, the others may serve a regulatory
CC function.
CC -1- SIMILARITY: Belongs to the dynein heavy chain family.
CC -----
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CC -----
CC EMBL; L31504; AAA64908.1; -;
DR EMBL; AABX01000204; EAA33380.1; -;
DR PIR; B54802; B54802.
DR InterPro; IPR003593; AAA ATPase.
DR InterPro; IPR004273; Dynein heavy.
DR Pfam; PF03028; Dynein heavy; 1.
DR SMART; SM00382; AAA; 3.
KW ATP-binding; Coiled coil; Dynein; Microtubule; Motor protein; Repeat.
FT DOMAIN 1 1904 Stem (By similarity).
FT DOMAIN 1905 2130 AAA 1 (By similarity).
FT DOMAIN 2202 2460 AAA 2 (By similarity).
FT DOMAIN 2566 2815 AAA 3 (By similarity).
FT DOMAIN 2909 3179 AAA 4 (By similarity).
FT DOMAIN 3193 3481 Stalk (By similarity).
FT DOMAIN 3565 3794 AAA 5 (By similarity).
FT DOMAIN 4003 4215 AAA 6 (By similarity).
FT DOMAIN 676 693 Coiled coil (Potential).
FT DOMAIN 1176 1215 Coiled coil (Potential).
FT DOMAIN 1327 1351 Coiled coil (Potential).
FT DOMAIN 1557 1574 Coiled coil (Potential).

FT DOMAIN 1637 1668 Coiled coil (Potential).
FT DOMAIN 2195 2218 Coiled coil (Potential).
FT DOMAIN 3193 3296 Coiled coil (Potential).
FT DOMAIN 3423 3481 Coiled coil (Potential).
FT DOMAIN 3778 3809 Coiled coil (Potential).
FT NP_BIND 1943 1950 ATP (Potential).
FT NP_BIND 2240 2247 ATP (Potential).
FT NP_BIND 2605 2612 ATP (Potential).
FT NP_BIND 2947 2954 ATP (Potential).
SQ SEQUENCE 4367 AA; 495568 MW; 1E10F3E2D170D6DF CRC64;

Query Match 69.0%; Score 40; DB 1; Length 4367;
Best Local Similarity 66.7%; Pred. No. 9.3e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 AWDDSLSEF 10
|||:|:|
DB 455 AWDESIKEF 463

RESULT 15

ID Q87GV3 PRELIMINARY; PRT; 182 AA.
AC Q87GV3;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein VPA1212.
GN OrderedLocNames=VPA1212;
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=670;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RIMD 2210633 / Serotype O3:K6;
RX MEDLINE=22508454; PubMed=12620739; DOI=10.1016/S0140-6736(03)12659-1;
RA Makino K., Oshima K., Kurokawa K., Yokoyama K., Uda T., Tagomori K.,
RA Iijima Y., Najiima M., Nakano M., Yamashita A., Kubota Y., Kimura S.,
RA Yasunaga T., Honda T., Shingawa H., Hattori M., Iida T.;
RT "Genome sequence of Vibrio parahaemolyticus: a pathogenic mechanism
distinct from that of V. cholerae."
RL Lancet 361:743-749(2003).
DR EMBL; AP005088; BAC62555.1; --
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 182 AA; 21333 MW; 2559BEC89FD78332 CRC64;

Query Match 67.2%; Score 39; DB 2; Length 182;
Best Local Similarity 50.0%; Pred. No. 47;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 AAWDDSLSEF 10
:|:|:|:|:|
DB 27 SSWDDNLQTF 36

Search completed: October 14, 2005, 16:19:59
Job time : 75.2188 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 14, 2005, 16:00:04 ; Search time 21.6562 Seconds
(without alignments)
37.917 Million cell updates/sec

Title: US-10-614-959-15
Perfect score: 58
Sequence: 1 AAWDSLSEFL 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA.*
1: /cgm2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgm2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgm2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgm2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgm2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgm2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	58	100.0	11	4	US-09-383-667-15
2	58	100.0	104	2	US-08-273-146-63
3	58	100.0	111	2	US-08-652-816A-15
4	46	79.3	11	4	US-08-350-260A-374
5	46	79.3	11	4	US-09-104-337A-374
6	44	75.9	11	2	US-08-350-260A-346
7	44	75.9	11	4	US-09-104-337A-346
8	43	74.1	9	2	US-08-665-202-60
9	43	74.1	9	4	US-09-315-574-60
10	43	74.1	10	2	US-08-350-260A-339
11	43	74.1	10	2	US-08-350-260A-497
12	43	74.1	10	4	US-09-104-337A-339
13	43	74.1	10	4	US-09-104-337A-497
14	43	74.1	11	2	US-08-350-260A-441
15	43	74.1	11	2	US-08-665-202-6
16	43	74.1	11	4	US-09-104-337A-441
17	43	74.1	11	4	US-09-315-574-6
18	43	74.1	98	2	US-08-211-202-111
19	43	74.1	98	2	US-08-665-202-38
20	43	74.1	98	4	US-09-315-574-38
21	43	74.1	109	3	US-09-240-274-59
22	43	74.1	110	3	US-09-240-274-60
23	43	74.1	111	2	US-08-665-202-36
24	43	74.1	111	2	US-08-665-202-43
25	43	74.1	111	4	US-09-315-574-36
26	43	74.1	111	4	US-09-315-574-43
27	43	74.1	112	2	US-08-665-202-39

28	43	74.1	112	4	US-09-315-574-39
29	43	74.1	113	1	US-08-211-202-112
30	43	74.1	113	1	US-08-211-202-113
31	43	74.1	113	1	US-08-211-202-114
32	43	74.1	258	2	US-08-665-202-5
33	43	74.1	258	4	US-09-315-574-5
34	43	74.1	262	3	US-09-063-821-4
35	43	74.1	262	4	US-09-956-086-4
36	43	74.1	262	4	US-09-956-087-4
37	43	74.1	282	3	US-09-420-592A-7
38	43	74.1	282	4	US-09-985-442-7
39	43	74.1	282	4	US-09-983-580-7
40	41	70.7	111	2	US-08-665-202-40
41	41	70.7	111	4	US-09-315-574-40
42	40	69.0	10	2	US-08-350-260A-361
43	40	69.0	10	2	US-08-350-260A-446
44	40	69.0	10	2	US-08-350-260A-514
45	40	69.0	10	4	US-09-104-337A-361

ALIGNMENTS

RESULT 1
US-09-383-667-15
; Sequence 15, Application US/09383667
; Patent No. 6624295
; GENERAL INFORMATION:
; APPLICANT: Adams, Camelia W.
; APPLICANT: Devaux, Brigitte
; APPLICANT: Eaton, Dan L.
; APPLICANT: Hass, Philip E.
; APPLICANT: Judice, J. Kevin
; APPLICANT: Kirchofer, Daniel
; APPLICANT: Suggett, Shelley
; TITLE OF INVENTION: Human Anti-Factor IX/IXa Antibodies
; FILE REFERENCE: P1661R2
; CURRENT APPLICATION NUMBER: US/09/383.667
; CURRENT FILING DATE: 1999-08-26
; EARLIER APPLICATION NUMBER: US 60/098,233
; EARLIER FILING DATE: 1998-08-28
; EARLIER APPLICATION NUMBER: US 60/122,767
; EARLIER FILING DATE: 1999-03-03
; NUMBER OF SEQ ID NOS: 32
; SEQ ID NO 15
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-383-667-15

Query Match 100.0%; Score 58; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.00037;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AAWDSLSEFL 11
Db 1 AAWDSLSEFL 11

RESULT 2
US-08-273-146-63
; Sequence 63, Application US/08273146
; Patent No. 5855885
; GENERAL INFORMATION:
; APPLICANT: Smith, Rodger
; APPLICANT: McCafferty, John
; APPLICANT: Chiswell, David
; APPLICANT: Darsley, Michael J.
; APPLICANT: Fitzgerald, Kevin
; APPLICANT: Kenten, John H.
; APPLICANT: Martin, Mark T.
; APPLICANT: Titmas, Richard C.
; APPLICANT: Williams, Richard O.

;; TITLE OF INVENTION: The Isolation and Production of
;; TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
;; NUMBER OF SEQUENCES: 71
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: IGEN, Inc.
;; STREET: 1530 East Jefferson St.
;; CITY: Rockville
;; STATE: MD
;; COUNTRY: USA
;; ZIP: 20852

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/273,146
;; FILING DATE: 14-JUL-1994
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ryan, John W.
;; REGISTRATION NUMBER: 33,771
;; REFERENCE/DOCKET NUMBER: 09000
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 301-984-8000
;; TELEFAX: 301-230-0158

;; INFORMATION FOR SEQ ID NO: 63:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 104 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
US-08-273-146-63

Query Match 100.0%; Score 58; DB 2; Length 104;

Best Local Similarity 100.0%; Pred. No. 0.0041;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDDSLSEFL 11

Db 83 AAWDDSLSEFL 93

|||||

RESULT 3

US-08-816A-15

; Sequence 15, Application US/0852816A

; Patent No. 5872215

; GENERAL INFORMATION:

; APPLICANT: Osbourn, JK

; APPLICANT: Allen, DJ

; APPLICANT: McCafferty, JG

; TITLE OF INVENTION: Specific binding members, materials and

; TITLE OF INVENTION: methods.

; NUMBER OF SEQUENCES: 53

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: United States of America

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/652,816A

; FILING DATE: 23-MAY-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9125579.4

; FILING DATE: 02-DEC-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9125579.8

; FILING DATE: 02-DEC-1991

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9206318.9

; FILING DATE: 24-MAR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9206372.6

; FILING DATE: 23-SEP-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9525004.9

; FILING DATE: 07-DEC-1995

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: GB 9610824.6

; FILING DATE: 23-MAY-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB92/02240

; FILING DATE: 02-DEC-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/244,597

; FILING DATE: 01-JUN-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: David W. Clough

; REGISTRATION NUMBER: 36,107

; REFERENCE/DOCKET NUMBER: 28111/33308

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 312-474-6300

; INFORMATION FOR SEQ ID NO: 15:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 111 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

US-08-652-816A-15

Query Match 100.0%; Score 58; DB 2; Length 111;

Best Local Similarity 100.0%; Pred. No. 0.0044;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDDSLSEFL 11

Db 90 AAWDDSLSEFL 100

|||||

RESULT 4

US-08-350-260A-374

; Sequence 374, Application US/08350260A

; Patent No. 5962255

; GENERAL INFORMATION:

; APPLICANT: Winter, Gregory Paul

; APPLICANT: Griffiths, Andrew David

; APPLICANT: Williams, Samuel Cameron

; APPLICANT: Waterhouse, Peter

; APPLICANT: Nissim, Ahuva

; APPLICANT: Johnson, Kevin Stuart

; APPLICANT: Smith, Andrew John Hammond

; TITLE OF INVENTION: Methods for producing members of specific

; TITLE OF INVENTION: binding pairs

; NUMBER OF SEQUENCES: 602

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: David W. Clough

; STREET: Marshall, O'Toole, Gerstein, Murray & Borun

; STREET: 6300 Sears Tower, 233 South Wacker Drive

; CITY: Chicago

; STATE: Illinois

; COUNTRY: USA

; ZIP: 60606-6402

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/350,260A

; FILING DATE: 05-DEC-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9110549.4
 ; FILING DATE: 15-MAY-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: GB 9206318.9
 ; FILING DATE: 24-MAR-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB91/01134
 ; FILING DATE: 10-JUL-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB92/00883
 ; FILING DATE: 15-MAY-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB93/00605
 ; FILING DATE: 24-MAR-1993
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/150,002
 ; FILING DATE: 31-MAR-1994
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/307,619
 ; FILING DATE: 16-SEP-1994
 ; NAME: Clough, David W
 ; REGISTRATION NUMBER: 36,107
 ; REFERENCE/DOCKET NUMBER: 28111/32372
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-474-6300
 ; INFORMATION FOR SEQ ID NO: 374:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; US-08-350-260A-374

Query Match 79.3%; Score 46; DB 2; Length 11;
 Best Local Similarity 72.7%; Pred. No. 0.05;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAWDDSLSEFL 11
 ||||| : :
 DB 1 AAWDDSLSAVV 11

RESULT 5
 US-09-104-337A-374
 ; Sequence 374, Application US/09104337A
 ; Patent No. 6492160
 ; GENERAL INFORMATION:
 ; APPLICANT: Winter, Gregory Paul
 ; Griffiths, Andrew David
 ; Williams, Samuel Cameron
 ; Waterhouse, Peter
 ; Nissim, Ahuva
 ; Johnson, Kevin Stuart
 ; Smith, Andrew John Hammond
 ; TITLE OF INVENTION: Methods for producing members of specific
 ; binding pairs
 ; NUMBER OF SEQUENCES: 600
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Audrey L. Bartnicki
 ; STREET: Marshall, Gerstein & Borun
 ; 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/104,337A
 ; FILING DATE: 25-Jun-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/350,260
 ; FILING DATE: 05-DEC-1994
 ; APPLICATION NUMBER: GB 9110549.4
 ; FILING DATE: 15-MAY-1991
 ; APPLICATION NUMBER: GB 9206318.9
 ; FILING DATE: 24-MAR-1992
 ; APPLICATION NUMBER: PCT/GB92/00883
 ; FILING DATE: 15-MAY-1992
 ; APPLICATION NUMBER: PCT/GB93/00605
 ; FILING DATE: 24-MAR-1993
 ; APPLICATION NUMBER: US 08/150,002
 ; FILING DATE: 31-MAR-1994
 ; APPLICATION NUMBER: US 08/307,619
 ; FILING DATE: 16-SEP-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bartnicki, Audrey L.
 ; REGISTRATION NUMBER: 40,499
 ; REFERENCE/DOCKET NUMBER: 28111/32372A
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-474-6300
 ; INFORMATION FOR SEQ ID NO: 374:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 11 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 374:
 ; US-09-104-337A-374

Query Match 79.3%; Score 46; DB 4; Length 11;
 Best Local Similarity 72.7%; Pred. No. 0.05;
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAWDDSLSEFL 11
 ||||| : :
 DB 1 AAWDDSLSAVV 11

RESULT 6
 US-08-350-260A-346
 ; Sequence 346, Application US/08350260A
 ; Patent No. 5962255
 ; GENERAL INFORMATION:
 ; APPLICANT: Winter, Gregory Paul
 ; Griffiths, Andrew David
 ; Williams, Samuel Cameron
 ; Waterhouse, Peter
 ; Nissim, Ahuva
 ; Johnson, Kevin Stuart
 ; Smith, Andrew John Hammond
 ; TITLE OF INVENTION: Methods for producing members of specific
 ; binding pairs
 ; NUMBER OF SEQUENCES: 602
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: David W. Clough
 ; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
 ; 6300 Sears Tower, 233 South Wacker Drive
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606-6402
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/350,260A
 ; FILING DATE: 05-DEC-1994
 ; CLASSIFICATION: 435

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9110549.4
;; FILING DATE: 15-MAY-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: GB 9206318.9
;; FILING DATE: 24-MAR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/GB91/01134
;; FILING DATE: 10-JUL-1991
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/GB92/00883
;; FILING DATE: 15-MAY-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/GB93/00605
;; FILING DATE: 24-MAR-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/150,002
;; FILING DATE: 31-MAR-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/307,619
;; FILING DATE: 16-SEP-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Clough, David W
;; REGISTRATION NUMBER: 36,107
;; REFERENCE/DOCKET NUMBER: 28111/32372
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312-474-6300
;; INFORMATION FOR SEQ ID NO: 346:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 11 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-350-260A-346

Query Match 75.9%; Score 44; DB 2; Length 11;
Best Local Similarity 72.7%; Pred. NO. 0.11;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAWDDSLSEFL 11
||| ||| : | :
DB 1 AAWDDSLAWFV 11

RESULT 7
US-09-104-337A-346
; Sequence 346, Application US/09104337A
; Patent No. 6492160
; GENERAL INFORMATION:

;; APPLICANT: Winter, Gregory Paul
;; Griffiths, Andrew David
;; Williams, Samuel Cameron
;; Waterhouse, Peter
;; Nissim, Ahuva
;; Johnson, Kevin Stuart
;; Smith, Andrew John Hammond
;; TITLE OF INVENTION: Methods for producing members of specific
;; binding pairs

;; NUMBER OF SEQUENCES: 600
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Audrey L. Bartnicki
;; STREET: Marshall, Gerstein & Borun
;; 6300 Sears Tower, 233 South Wacker Drive
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: USA
;; ZIP: 60606-6402

;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25 (BPO)
;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/104,337A
;; FILING DATE: 25-Jun-1998
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/350,260
;; FILING DATE: 05-DEC-1994
;; APPLICATION NUMBER: GB 9110549.4
;; FILING DATE: 15-MAY-1991
;; APPLICATION NUMBER: GB 9206318.9
;; FILING DATE: 24-MAR-1992
;; APPLICATION NUMBER: PCT/GB92/00883
;; FILING DATE: 15-MAY-1992
;; APPLICATION NUMBER: PCT/GB93/00605
;; FILING DATE: 24-MAR-1993
;; APPLICATION NUMBER: US 08/150,002
;; FILING DATE: 31-MAR-1994
;; APPLICATION NUMBER: US 08/307,619
;; FILING DATE: 16-SEP-1994
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bartnicki, Audrey L.
;; REGISTRATION NUMBER: 40,499
;; REFERENCE/DOCKET NUMBER: 28111/32372A
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312-474-6300
;; INFORMATION FOR SEQ ID NO: 346:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 11 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; SEQUENCE DESCRIPTION: SEQ ID NO: 346:
;; US-09-104-337A-346

Query Match 75.9%; Score 44; DB 4; Length 11;
Best Local Similarity 72.7%; Pred. No. 0.11;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 AAWDDSLSEFL 11
||| ||| : | :
DB 1 AAWDDSLAWFV 11

RESULT 8
US-08-665-202-60
; Sequence 60, Application US/08665202
; Patent No. 5977322
; GENERAL INFORMATION:
;; APPLICANT: Marks, James D.
;; APPLICANT: Schier, Robert
;; TITLE OF INVENTION: No. 5977322el High Affinity Human Antibodies to
;; Tumor Antigens
;; NUMBER OF SEQUENCES: 141
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend and Crew LLP
;; STREET: Two Embarcadero Center, Eighth Floor
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94111-3834
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/665,202
;; FILING DATE: 13-JUN-1996
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/000,238
;; FILING DATE: 14-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 60/000,250
;; FILING DATE: 15-JUN-1995

```
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061410
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-665-202-60

Query Match          74.1%; Score 43; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAWDDSLs 8
       |||||
Db       1 AAWDDSLs 8

RESULT 9
US-09-315-574-60
; Sequence 60, Application US/09315574
; Patent No. 6512097
; GENERAL INFORMATION:
; APPLICANT: Marks, James D.
; APPLICANT: Schier, Robert
; TITLE OF INVENTION: No. 6512097el High Affinity Human Antibodies to
; TITLE OF INVENTION: Tumor Antigens
; NUMBER OF SEQUENCES: 141
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Hsue P.C.
; STREET: Four Embarcadero Center, Suite 1100
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4106
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/315,574
; FILING DATE: 20-MAY-99
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,238
; FILING DATE: 14-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,250
; FILING DATE: 15-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/665,202
; FILING DATE: 13-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 02307E-061411
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 60:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
```

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; MOLECULE TYPE: peptide
US-09-315-574-60

Query Match          74.1%; Score 43; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 AAWDDSLs 8
       |||||
Db       1 AAWDDSLs 8

RESULT 10
US-08-350-260A-339
; Sequence 339, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 339:
; SEQUENCE CHARACTERISTICS:
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; SEQUENCE DESCRIPTION: SEQ ID NO: 497:
US-09-104-337A-497

Query Match          74.1%; Score 43; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDDSL 8
DB 1 AAWDDSL 8

RESULT 14
US-08-350-260A-441
; Sequence 441, Application US/08350260A
; Patent No. 5962255
; GENERAL INFORMATION:
; APPLICANT: Winter, Gregory Paul
; APPLICANT: Griffiths, Andrew David
; APPLICANT: Williams, Samuel Cameron
; APPLICANT: Waterhouse, Peter
; APPLICANT: Nissim, Ahuva
; APPLICANT: Johnson, Kevin Stuart
; APPLICANT: Smith, Andrew John Hammond
; TITLE OF INVENTION: Methods for producing members of specific
; TITLE OF INVENTION: binding pairs
; NUMBER OF SEQUENCES: 602
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David W. Clough
; STREET: Marshall, O'Tool, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/350,260A
; FILING DATE: 05-DEC-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9110549.4
; FILING DATE: 15-MAY-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9206318.9
; FILING DATE: 24-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB91/01134
; FILING DATE: 10-JUL-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB92/00883
; FILING DATE: 15-MAY-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB93/00605
; FILING DATE: 24-MAR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/150,002
; FILING DATE: 31-MAR-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/307,619
; FILING DATE: 16-SEP-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Clough, David W
; REGISTRATION NUMBER: 36,107
; REFERENCE/DOCKET NUMBER: 28111/32372
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; INFORMATION FOR SEQ ID NO: 441:
; SEQUENCE CHARACTERISTICS:

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Search completed: October 14, 2005, 16:22:03

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OM protein - protein search, using sw model

Run on: October 14, 2005, 16:20:10 ; Search time 78.2031 Seconds
(without alignments)
58.615 Million cell updates/sec

Title: US-10-614-959-15
Perfect score: 58
Sequence: 1 AAWDDSLSEFL 11

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Gapop 10.0 , Gapext 0.5

Searched: 1859788 seqs, 416717961 residues

Total number of hits satisfying chosen parameters: 1859788

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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3	58	100.0	243	10	US-09-880-748-1927
4	58	100.0	243	15	US-10-293-418-1927
5	58	100.0	243	18	US-10-981-692-29
6	58	100.0	243	18	US-10-981-692-33
7	58	100.0	244	18	US-10-981-692-26
8	58	100.0	245	10	US-09-880-748-1926
9	58	100.0	245	15	US-10-293-418-1926
10	58	100.0	245	15	US-10-293-418-3241
11	58	100.0	245	18	US-10-981-692-31

12	58	100.0	246	10	US-09-880-748-1913	Sequence 1913, Ap
13	58	100.0	246	10	US-09-880-748-1917	Sequence 1917, Ap
14	58	100.0	246	15	US-10-293-418-1913	Sequence 1913, Ap
15	58	100.0	246	15	US-10-293-418-1917	Sequence 1917, Ap
16	58	100.0	247	10	US-09-880-748-1443	Sequence 1443, Ap
17	58	100.0	247	10	US-09-880-748-1682	Sequence 1682, Ap
18	58	100.0	247	10	US-09-880-748-1707	Sequence 1707, Ap
19	58	100.0	247	10	US-09-880-748-1899	Sequence 1899, Ap
20	58	100.0	247	10	US-09-880-748-1928	Sequence 1928, Ap
21	58	100.0	247	10	US-09-880-748-1934	Sequence 1934, Ap
22	58	100.0	247	15	US-10-293-418-1443	Sequence 1443, Ap
23	58	100.0	247	15	US-10-293-418-1682	Sequence 1682, Ap
24	58	100.0	247	15	US-10-293-418-1707	Sequence 1707, Ap
25	58	100.0	247	15	US-10-293-418-1899	Sequence 1899, Ap
26	58	100.0	247	15	US-10-293-418-1928	Sequence 1928, Ap
27	58	100.0	247	15	US-10-293-418-1934	Sequence 1934, Ap
28	58	100.0	247	17	US-10-935-290-46	Sequence 46, Appl
29	58	100.0	247	17	US-10-935-290-88	Sequence 88, Appl
30	58	100.0	247	18	US-10-981-692-27	Sequence 27, Appl
31	58	100.0	247	18	US-10-981-692-37	Sequence 37, Appl
32	58	100.0	247	20	US-11-046-857-44	Sequence 44, Appl
33	58	100.0	248	18	US-10-981-692-39	Sequence 39, Appl
34	58	100.0	249	10	US-09-880-748-1419	Sequence 1419, Ap
35	58	100.0	249	10	US-09-880-748-1618	Sequence 1618, Ap
36	58	100.0	249	10	US-09-880-748-2049	Sequence 2049, Ap
37	58	100.0	249	10	US-09-880-748-2065	Sequence 2065, Ap
38	58	100.0	249	15	US-10-293-418-1419	Sequence 1419, Ap
39	58	100.0	249	15	US-10-293-418-1618	Sequence 1618, Ap
40	58	100.0	249	15	US-10-293-418-2049	Sequence 2049, Ap
41	58	100.0	249	15	US-10-293-418-2065	Sequence 2065, Ap
42	58	100.0	249	20	US-11-017-030-14	Sequence 14, Appl
43	58	100.0	250	18	US-10-981-692-22	Sequence 22, Appl
44	58	100.0	250	20	US-11-090-847-84	Sequence 84, Appl
45	58	100.0	251	10	US-09-880-748-1309	Sequence 1309, Ap

ALIGNMENTS

RESULT 1
US-10-981-692-24
; Sequence 24, Application US/10981692
; Publication No. US20050163777A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PFS90P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; PCT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N015E08 scFv
US-10-981-692-24

Query Match 100.0%; Score 58; DB 18; Length 242;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AAWDDSLSEFL 11
DB 221 AAWDDSLSEFL 231
RESULT 2

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US-10-981-692-40
; Sequence 40, Application US/10981692
; Publication No. US20050163777A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PF590P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; PRIOR FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 242
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N015D10 scFv
US-10-981-692-40

Query Match      100.0%; Score 58; DB 18; Length 242;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDDSLSEFL 11
Db 221 AAWDDSLSEFL 231

RESULT 3
US-09-880-748-1927
; Sequence 1927, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1927
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1927

Query Match      100.0%; Score 58; DB 10; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDDSLSEFL 11
Db 222 AAWDDSLSEFL 232

RESULT 4
US-10-293-418-1927
; Sequence 1927, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1927
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1927

Query Match      100.0%; Score 58; DB 15; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDDSLSEFL 11
Db 222 AAWDDSLSEFL 232

RESULT 5
US-10-981-692-29
; Sequence 29, Application US/10981692
; Publication No. US20050163777A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PF590P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N024E07 scFv
US-10-981-692-29

Query Match      100.0%; Score 58; DB 18; Length 243;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AAWDDSLSEFL 11
Db 222 AAWDDSLSEFL 232

RESULT 6
US-10-981-692-33
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; Sequence 33, Application US/10981692
; Publication No. US20050163777A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PF590P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 33
; LENGTH: 243
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N023E01 scFv
US-10-981-692-33

Query Match      100.0%; Score 58; DB 18; Length 243;
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Matches 11; Conservative 0; Mismatches 0;

QY      1 AAWDDSLSEFL 11
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DB      222 AAWDDSLSEFL 232

RESULT 7
US-10-981-692-26
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; Publication No. US20050163777A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PF590P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 244
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N024D01 scFv
US-10-981-692-26

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Best Local Similarity 100.0%; Pred. No. 0.048; 0; Indels 0; Gaps 0;
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DB      223 AAWDDSLSEFL 233

RESULT 8
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; Publication No. US20030059937A1
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; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
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; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
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; ORGANISM: Homo sapiens
US-09-880-748-1926

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Matches 11; Conservative 0; Mismatches 0;

QY      1 AAWDDSLSEFL 11
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DB      224 AAWDDSLSEFL 234

RESULT 9
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; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1926
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1926

Query Match      100.0%; Score 58; DB 15; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.048; 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0;

QY      1 AAWDDSLSEFL 11
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DB      224 AAWDDSLSEFL 234

RESULT 10
US-10-293-418-3241
; Sequence 3241, Application US/10293418
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; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3241
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-3241
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Query Match 100.0%; Score 58; DB 15; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AAWDDSLSEFL 11
Db 224 AAWDDSLSEFL 234
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RESULT 11
US-10-981-692-31
; Sequence 31, Application US/10981692
; Publication No. US20050163777A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to Neurokinin B
; FILE REFERENCE: PF590P1
; CURRENT APPLICATION NUMBER: US/10/981,692
; CURRENT FILING DATE: 2004-11-05
; PRIOR APPLICATION NUMBER: PCT/US03/16802
; PRIOR FILING DATE: 2003-05-29
; PRIOR APPLICATION NUMBER: 60/383,802
; PRIOR FILING DATE: 2002-05-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 31
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: N024D08 scFv
US-10-981-692-31
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Query Match 100.0%; Score 58; DB 18; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 AAWDDSLSEFL 11
Db 224 AAWDDSLSEFL 234
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RESULT 12

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US-09-880-748-1913
; Sequence 1913, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1913
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1913
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Best Local Similarity 100.0%; Pred. No. 0.049; 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0;
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Db 225 AAWDDSLSEFL 235
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RESULT 13
US-09-880-748-1917
; Sequence 1917, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1917
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1917
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Query Match 100.0%; Score 58; DB 10; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.049; 0; Indels 0; Gaps 0;
Matches 11; Conservative 0; Mismatches 0;
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QY 1 AAWDDSLSEFL 11
Db 225 AAWDDSLSEFL 235
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RESULT 14

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US-10-293-418-1913
; Sequence 1913, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1913
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1913
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Query Match      100.0%; Score 58; DB 15; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 AAWDDSLSEFL 11
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Db      225 AAWDDSLSEFL 235
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RESULT 15

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US-10-293-418-1917
; Sequence 1917, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1917
; LENGTH: 246
; TYPE: PRT
; ORGANISM: Homo sapiens
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US-10-293-418-1917

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Query Match      100.0%; Score 58; DB 15; Length 246;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 AAWDDSLSEFL 11
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Db      225 AAWDDSLSEFL 235
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Search completed: October 14, 2005, 17:00:44
Job time : 78.2031 secs

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